

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Daggett, Lorrie P.
Ellis, Steven B.
Liaw, Chen W.
Lu, Chin-Chun
- (ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
SUBUNITS, DNA ENCODING SAME AND USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 - (B) STREET: 444 South Flower Street, Suite 2000
 - (C) CITY: Los Angeles
 - (D) STATE: CA
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 90071-2921
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 20-APR-1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/052,449
 - (B) FILING DATE: 20-APR-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Reiter, Stephen E.
 - (B) REGISTRATION NUMBER: 31,192
 - (C) REFERENCE/DOCKET NUMBER: P41 9424
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 619-546-4737
 - (B) TELEFAX: 619-546-9392

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 262..3078

1000744-12001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC GCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGGCCG GGCGAGCGCA	180
GGACGGCCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCCG GGGCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
1 5	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	25
15 20	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
30 35	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	55
45 50	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	70
60 65	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	90
75 80 85	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	105
95 100	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	120
110 115	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	135
125 130	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	150
140 145	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	170
155 160 165	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	185
175 180	
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG	867
Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	200
190 195	
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC	915
Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	215
205 210	

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ATC Ile 220	ATC Ile 220	CTT Leu	TCT Ser	GCC Ala	AGC Ser	GAG Glu 225	GAC Asp	GAT Asp	GCT Ala	GCC Ala	ACT Thr 230	GTA Val	TAC Tyr	CGC Arg	GCA Ala	963
GCC Ala 235	GCG Ala	ATG Met	CTG Leu	AAC Asn 240	ATG Met	ACG Thr	GGC Gly	TCC Ser	GGG Gly 245	TAC Tyr	GTG Val	TGG Trp	CTG Leu	GTC Val	GGC Gly 250	1011
GAG Glu	CGC Arg	GAG Glu	ATC Ile	TCG Ser 255	GGG Gly	AAC Asn	GCC Ala	CTG Leu	CGC Arg 260	TAC Tyr	GCC Ala	CCA Pro	GAC Asp	GGC Gly 265	ATC Ile	1059
CTC Leu	GGG Gly	CTG Leu	CAG Gln 270	CTC Leu	ATC Ile	AAC Asn	GGC Gly	AAG Lys 275	AAC Asn	GAG Glu	TCG Ser	GCC Ala	CAC His 280	ATC Ile	AGC Ser	1107
GAC Asp	GCC Ala	GTG Val 285	GGC Gly	GTG Val	GTG Val	GCC Ala	CAG Gln 290	GCC Ala	GTG Val	CAC His	GAG Glu	CTC Leu 295	CTC Leu	GAG Glu	AAG Lys	1155
GAG Glu 300	AAC Asn	ATC Ile	ACC Thr	GAC Asp	CCG Pro	CCG Pro	CGG Arg	GGC Gly	TGC Cys	GTG Val	GGC Gly 310	AAC Asn	ACC Thr	AAC Asn	ATC Ile	1203
TGG Trp 315	AAG Lys	ACC Thr	GGG Gly	CCG Pro	CTC Leu 320	TTC Phe	AAG Lys	AGA Arg	GTG Val	CTG Leu 325	ATG Met	TCT Ser	TCC Ser	AAG Lys	TAT Tyr 330	1251
CGC Ala	GAT Asp	GGG Gly	GTG Val	ACT Thr 335	GCT Gly	CGC Arg	GTG Val	GAG Glu	TTC Phe 340	AAT Asn	GAG Glu	GAT Asp	GGG Gly	GAC Asp 345	CGG Arg	1299
AAG Lys	TTC Phe	GCC Ala	AAC Asn 350	TAC Tyr	AGC Ser	ATC Ile	ATG Met	AAC Asn 355	CTG Leu	CAG Gln	AAC Asn	CGC Arg	AAG Lys 360	CTG Leu	GTG Val	1347
CAA Gln	GTG Val	GGC Gly 365	ATC Ile	TAC Tyr	AAT Asn	GGC Gly	ACC Thr 370	CAC His	GTC Val	ATC Ile	CCT Pro	AAT Asn 375	GAC Asp	AGG Arg	AAG Lys	1395
ATC Ile 380	ATC Ile	TGG Trp	CCA Pro	GGC Gly	GGA Gly	GAG Glu 385	ACA Thr	GAG Glu	AAG Lys	CCT Pro	CGA Arg 390	GGG Gly	TAC Tyr	CAG Gln	ATG Met	1443
TCC Ser 395	ACC Thr	AGA Arg	CTG Leu	AAG Lys	ATT Ile 400	GTG Val	ACG Thr	ATC Ile	CAC His	CAG Gln 405	GAG Glu	CCC Pro	TTC Phe	GTG Val	TAC Tyr 410	1491
GTC Val	AAG Lys	CCC Pro	ACG Thr	CTG Leu 415	AGT Ser	GAT Asp	GGG Gly	ACA Thr	TGC Cys 420	AAG Lys	GAG Glu	GAG Glu	TTC Phe	ACA Thr 425	GTC Val	1539
AAC Asn	GGC Gly	GAC Asp	CCA Pro 430	GTC Val	AAG Lys	AAG Lys	GTG Val 435	ATC Ile	TGC Cys	ACC Thr	GGG Gly	CCC Pro	AAC Asn 440	GAC Asp	ACG Thr	1587
TCG Ser	CCG Pro	GGC Gly 445	AGC Ser	CCC Pro	CGC Arg	CAC His	ACG Thr 450	GTG Val	CCT Pro	CAG Gln	TGT Cys	TGC Cys 455	TAC Tyr	GGC Gly	TTT Phe	1635
TGC Cys 460	ATC Ile	GAC Asp	CTG Leu	CTC Leu	ATC Ile	AAG Lys 465	CTG Leu	GCA Ala	CGG Arg	ACC Thr	ATG Met 470	AAC Asn	TTC Phe	ACC Thr	TAC Tyr	1683
GAG Glu 475	GTG Val	CAC His	CTG Leu	GTG Val	GCA Ala 480	GAT Asp	GGC Gly	AAG Lys	TTC Phe	GGC Gly 485	ACA Thr	CAG Gln	GAG Glu	CGG Arg	GTG Val 490	1731

1000747-120701

AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu 495 500 505	1779
AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu 510 515 520	1827
CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu 525 530 535	1875
ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe 540 545 550	1923
ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val 555 560 565 570	1971
CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe 575 580 585	2019
GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAG GAC GCA CTG ACC Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Glu Asp Ala Leu Thr 590 595 600	2067
CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly 605 610 615	2115
ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met 620 625 630	2163
GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn 635 640 645 650	2211
CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly 655 660 665	2259
ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala 670 675 680	2307
ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu 685 690 695	2355
CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala 700 705 710	2403
GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile 715 720 725 730	2451
TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu 735 740 745	2499
GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met 750 755 760	2547

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CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG	2595
Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys	
765 770 775	
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG	2643
Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg	
780 785 790	
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT	2691
Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe	
795 800 805 810	
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC	2739
Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala	
815 820 825	
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT	2787
Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp	
830 835 840	
GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG	2835
Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Val Asn Val Trp	
845 850 855	
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT	2883
Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro	
860 865 870	
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC	2931
Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser	
875 880 885 890	
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC	2979
Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg	
895 900 905	
GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT	3027
Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile	
910 915 920	
GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC	3075
Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser	
925 930 935	
TGAGACTCCC CGCCCGCCCT CCTCTGCCCC CTCCCCCGCA GACAGACAGA CAGACGGACG	3135
GGACAGCGGC CCGGCCACG CAGAGCCCCG GAGCACCACG GGGTCGGGGG AGGAGCACCC	3195
CCAGCCTCCC CCAGGCTGCG CCTGCCCGCC CGCCGGTTGG CCGGCTGGCC GGTCCACCCC	3255
GTCCCGGCCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGCTCT GTGTATTTCT	3315
ATTTTGCAGC AGTACCATCC CACTGATATC ACGGGCCCGC TCAACCTCTC AGATCCCTCG	3375
GTCAGCACCG TGGTGTGAGG CCCCCGAGG CGCCACCTG CCCAGTTAGC CCGGCCAAGG	3435
ACACTGATGG GTCCTGCTGC TCGGGAAGGC CTGAGGGAAG CCCACCCGCC CCAGAGACTG	3495
CCCACCTTGG GCCTCCCGTC CGTCCGCCCC CCCACCCCGC TGCCTGGCGG GCAGCCCCTG	3555
CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC GGCTGGGCAG	3615
GGCCGCAGGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG GGGAGCGGGG	3675
GCTAACTGCC CCCAGGCGGA GGGGCTTGA GCAGAGACGG CAGCCCCATC CTTCCCGCAG	3735
CACCAGCCTG AGCCACAGTG GGGCCCATGG CCCCAGCTGG CTGGGTGCGC CCTCCTCGGG	3795

10007747-120704

CGCCTGCGCT CCTCTGCAGC CTGAGCTCCA CCCTCCCCTC TTCTTGCGGC ACCGCCACCC 3855
 AAACACCCCG TCTGCCCCCTT GACGCCACAC GCCGGGGCTG GCGCTGCCCT CCCCCACGGC 3915
 CGTCCCTGAC TTCCAGCTG GCAGCGCCTC CCGCCGCCTC GGGCCGCCTC CTCCAGAATC 3975
 GAGAGGGCTG AGCCCCCTCT CTCCTCGTCC GGCCTGCAGC ACAGAAGGGG GCCTCCCCGG 4035
 GGGTCCCCCG ACGCTGGCTC GGGACTGTCT TCAACCCTGC CCTGCACCTT GGGCACGGGA 4095
 GAGCGCCACC CGCCCGCCCC CGCCCTCGCT CCGGGTGCGT GACCGGCCCCG CCACCTTGTA 4155
 CAGAACCAGC ACTCCCAGGG CCCGAGCGCG TGCCTTCCCC GTGCGCAGCC GCGCTCTGCC 4215
 CCTCCGTCCC CAGGGTGCGAG GCGCGCACCG CCCAACCCCC ACCTCCCGGT GTATGCAGTG 4275
 GTGATGCCTA AAGGAATGTC ACG 4298

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 938 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser
 1 5 10 15
 Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val
 20 25 30
 Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln
 35 40 45
 Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser
 50 55 60
 Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu
 65 70 75 80
 Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro
 85 90 95
 Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly
 100 105 110
 Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr
 115 120 125
 Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr
 130 135 140
 Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp
 145 150 155 160
 Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala
 165 170 175
 Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu
 180 185 190

T000744-120701

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu
 195 200 205
 Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser
 210 215 220
 Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met
 225 230 235 240
 GlyThr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser
 245 250 255
 Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile
 260 265 270
 Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val
 275 280 285
 Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro
 290 295 300
 Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu
 305 310 315 320
 Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly
 325 330 335
 Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser
 340 345 350
 Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn
 355 360 365
 Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly
 370 375 380
 Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile
 385 390 395 400
 Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser
 405 410 415
 Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys
 420 425 430
 Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg
 435 440 445
 His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile
 450 455 460
 Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala
 465 470 475 480
 Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys
 485 490 495
 Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met
 500 505 510
 Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu
 515 520 525
 Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys
 530 535 540

Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser
 545 550 555 560
 Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met
 565 570 575
 Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn
 580 585 590
 Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp
 595 600 605
 Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro
 610 615 620
 Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala
 625 630 635 640
 Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val
 645 650 655
 Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu
 660 665 670
 Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser
 675 680 685
 Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg
 690 695 700
 His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala
 705 710 715 720
 Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu
 725 730 735
 Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu
 740 745 750
 Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp
 755 760 765
 Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe
 770 775 780
 Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser
 785 790 795 800
 Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val
 805 810 815
 Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe
 820 825 830
 Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met
 835 840 845
 Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp
 850 855 860
 Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe
 865 870 875 880
 Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser
 885 890 895

10007747 "120701
 74720007

Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg Gly Ala Leu Gln Asn Gln
 900 905 910

Lys Asp Thr Val Leu Pro Arg Arg Ala Ile Glu Arg Glu Glu Gly Gln
 915 920 925

Leu Gln Leu Cys Ser Arg His Arg Glu Ser
 930 935

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG TCC TAT GAC AAC	48
Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn	
1 5 10 15	
AAG CGC GGA CCC AAG	63
Lys Arg Gly Pro Lys	
20	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn
1 5 10 15
Lys Arg Gly Pro Lys
20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10007747 "120701"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 189..3899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCTTAATAA GATTTGCCAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC	374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC	422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC	470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC	518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT	566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG	614
Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA	662
Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC	710
Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CCG GCC GTC GCC GAC GCC AGC CAC	758
His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	
175 180 185 190	
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA	806
Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly	
195 200 205	

T0007747 120701

GGG	CCG	CGC	GCG	CGC	ACG	CAG	CGC	CTG	CTG	CGC	CAG	CTC	GAC	GCG	CCC	854
Gly	Pro	Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro	
			210					215					220			
GTG	TTT	GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	CTC	TTC	GCC	902
Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	
		225					230					235				
GAG	GCG	GCG	CAG	GCC	GGT	CTG	GTG	GGG	CCC	GGC	CAC	GTG	TGG	CTG	GTG	950
Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	
	240					245					250					
CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	ACC	TTC	CCC	998
Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	
255					260					265					270	
GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC	1046
Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	
				275					280					285		
CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC	1094
Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	
			290					295					300			
TAC	TGG	CGC	CAG	CAT	GGA	ACC	CTG	CCA	GCC	CCG	GCC	GGG	GAC	TGC	CGT	1142
Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	
		305					310					315				
GTT	CAC	CCT	GGG	CCC	GTC	AGC	CCT	GCC	CGG	GAG	GCC	TTC	TAC	AGG	CAC	1190
Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	
	320					325					330					
CTA	CTG	AAT	GTC	ACC	TGG	GAG	GGC	CGA	GAC	TTC	TCC	TTC	AGC	CCT	GGT	1238
Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	
335					340				345						350	
GGG	TAC	CTG	GTC	CAG	CCC	ACC	ATG	GTG	GTG	ATC	GCC	CTC	AAC	CGG	CAC	1286
Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	
				355				360						365		
CGC	CTC	TGG	GAG	ATG	GTG	GGG	CGC	TGG	GAG	CAT	GGC	GTC	CTA	TAC	ATG	1334
Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	
			370					375					380			
AAG	TAC	CCC	GTG	TGG	CCT	CGC	TAC	AGT	GCC	TCT	CTG	CAG	CCT	GTG	GTG	1382
Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	
		385					390					395				
GAC	AGT	CGG	CAC	CTG	ACG	GTG	GCC	ACG	CTG	GAA	GAG	CGG	CCC	TTT	GTC	1430
Asp	Ser	Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	
	400					405					410					
ATC	GTG	GAG	AGC	CCT	GAC	CCT	GGC	ACA	GGA	GGC	TGT	GTC	CCC	AAC	ACC	1478
Ile	Val	Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	
415					420					425					430	
GTG	CCC	TGC	CGC	AGG	CAG	AGC	AAC	CAC	ACC	TTC	AGC	AGC	GGG	GAC	GTG	1526
Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	
				435					440					445		
GCC	CCC	TAC	ACC	AAG	CTC	TGC	TGT	AAG	GGA	TTC	TGC	ATC	GAC	ATC	CTC	1574
Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	
			450					455					460			
AAG	AAG	CTG	GCC	AGA	GTG	GTC	AAA	TTC	TCC	TAC	GAC	CTG	TAC	CTG	GTG	1622
Lys	Lys	Leu	Ala	Arg	Val	Val	Lys	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	
		465					470					475				

T0007747 120701

ACC	AAC	GGC	AAG	CAT	GGC	AAG	CGG	GTG	CGC	GGC	GTA	TGG	AAC	GGC	ATG	1670
Thr	Asn	Gly	Lys	His	Gly	Lys	Arg	Val	Arg	Gly	Val	Trp	Asn	Gly	Met	
	480					485					490					
ATT	GGG	GAG	GTG	TAC	TAC	AAG	CGG	GCA	GAC	ATG	GCC	ATC	GGC	TCC	CTC	1718
Ile	Gly	Glu	Val	Tyr	Tyr	Lys	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	
495					500					505					510	
ACC	ATC	AAT	GAG	GAA	CGC	TCC	GAG	ATC	GTA	GAC	TTC	TCT	GTA	CCC	TTT	1766
Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	
				515					520					525		
GTG	GAG	ACG	GGC	ATC	AGT	GTG	ATG	GTG	GCT	CGC	AGC	AAT	GGC	ACC	GTC	1814
Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	
			530					535					540			
TCC	CCC	TCG	GCC	TTC	TTG	GAG	CCA	TAT	AGC	CCT	GCA	GTG	TGG	GTG	ATG	1862
Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	
		545					550					555				
ATG	TTT	GTC	ATG	TGC	CTC	ACT	GTG	GTG	GCC	ATC	ACC	GTC	TTC	ATG	TTC	1910
Met	Phe	Val	Met	Cys	Leu	Thr	Val	Val	Ala	Ile	Thr	Val	Phe	Met	Phe	
	560					565					570					
GAG	TAC	TTC	AGC	CCT	GTC	AGC	TAC	AAC	CAG	AAC	CTC	ACC	AGA	GGC	AAG	1958
Glu	Tyr	Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln	Asn	Leu	Thr	Arg	Gly	Lys	
575					580					585					590	
AAG	TCC	GGG	GGC	CCA	GCT	TTC	ACT	ATC	GGC	AAG	TCC	GTG	TGG	CTG	CTG	2006
Lys	Ser	Gly	Gly	Pro	Ala	Phe	Thr	Ile	Gly	Lys	Ser	Val	Trp	Leu	Leu	
				595					600					605		
TGG	GCG	CTG	GTC	TTC	AAC	AAC	TCA	GTG	CCC	ATC	GAG	AAC	CCG	CGG	GGC	2054
Trp	Ala	Leu	Val	Phe	Asn	Asn	Ser	Val	Pro	Ile	Glu	Asn	Pro	Arg	Gly	
			610					615					620			
ACC	ACC	AGC	AAG	ATC	ATG	GTT	CTG	GTC	TGG	GCC	TTC	TTT	GCT	GTC	ATC	2102
Thr	Thr	Ser	Lys	Ile	Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	
		625					630					635				
TTC	CTC	GCC	AGA	TAC	ACG	GCC	AAC	CTG	GCC	GCC	TTC	ATG	ATC	CAA	GAG	2150
Phe	Leu	Ala	Arg	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	
	640					645					650					
CAA	TAC	ATC	GAC	ACT	GTG	TCG	GGC	CTC	AGT	GAC	AAG	AAG	TTT	CAG	CGG	2198
Gln	Tyr	Ile	Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	
655					660					665					670	
CCT	CAA	GAT	CAG	TAC	CCA	CCT	TTC	CGC	TTC	GGC	ACG	GTG	CCC	AAC	GGC	2246
Pro	Gln	Asp	Gln	Tyr	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	
				675					680					685		
AGC	ACG	GAG	CGG	AAC	ATC	CGC	AGT	AAC	TAC	CGT	GAC	ATG	CAC	ACC	CAC	2294
Ser	Thr	Glu	Arg	Asn	Ile	Arg	Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	
			690					695					700			
ATG	GTC	AAG	TTC	AAC	CAG	CGC	TCG	GTG	GAG	GAC	GCG	CTC	ACC	AGC	CTC	2342
Met	Val	Lys	Phe	Asn	Gln	Arg	Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	
		705					710					715				
AAG	ATG	GGG	AAG	CTG	GAT	GCC	TTC	ATC	TAT	GAT	GCT	GCT	GTC	CTC	AAC	2390
Lys	Met	Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	
	720					725					730					
TAC	ATG	GCA	GGC	AAG	GAC	GAG	GGC	TGC	AAG	CTG	GTC	ACC	ATT	GGG	TCT	2438
Tyr	Met	Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	
735					740					745					750	

GGC	AAG	GTC	TTT	GCT	ACC	ACT	GGC	TAC	GGC	ATC	GCC	ATG	CAG	AAG	GAC	2486
Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Met	Gln	Lys	Asp	
				755					760					765		
TCC	CAC	TGG	AAG	CGG	GCC	ATA	GAC	CTG	GCG	CTC	TTG	CAG	TTC	CTG	GGG	2534
Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	
			770					775					780			
GAC	GGA	GAG	ACA	CAG	AAA	CTG	GAG	ACA	GTG	TGG	CTC	TCA	GGG	ATC	TGC	2582
Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val	Trp	Leu	Ser	Gly	Ile	Cys	
		785					790					795				
CAG	AAT	GAG	AAG	AAC	GAG	GTG	ATG	AGC	AGC	AAG	CTG	GAC	ATC	GAC	AAC	2630
Gln	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Lys	Leu	Asp	Ile	Asp	Asn	
	800					805					810					
ATG	GCA	GGC	GTC	TTC	TAC	ATG	CTG	CTG	GTG	GCC	ATG	GGG	CTG	GCC	CTG	2678
Met	Ala	Gly	Val	Phe	Tyr	Met	Leu	Leu	Val	Ala	Met	Gly	Leu	Ala	Leu	
815					820					825					830	
CTG	GTC	TTC	GCC	TGG	GAG	CAC	CTG	GTC	TAC	TGG	AAG	CTG	CGC	CAC	TCG	2726
Leu	Val	Phe	Ala	Trp	Glu	His	Leu	Val	Tyr	Trp	Lys	Leu	Arg	His	Ser	
				835					840					845		
GTG	CCC	AAC	TCA	TCC	CAG	CTG	GAC	TTC	CTG	CTG	GCT	TTC	AGC	AGG	GGC	2774
Val	Pro	Asn	Ser	Ser	Gln	Leu	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	
			850					855					860			
ATC	TAC	AGC	TGC	TTC	AGC	GGG	GTG	CAG	AGC	CTC	GCC	AGC	CCA	CCG	CGG	2822
Ile	Tyr	Ser	Cys	Phe	Ser	Gly	Val	Gln	Ser	Leu	Ala	Ser	Pro	Pro	Arg	
		865					870					875				
CAG	GCC	AGC	CCG	GAC	CTC	ACG	GCC	AGC	TCG	GCC	CAG	GCC	AGC	GTG	CTC	2870
Gln	Ala	Ser	Pro	Asp	Leu	Thr	Ala	Ser	Ser	Ala	Gln	Ala	Ser	Val	Leu	
	880					885					890					
AAG	ATG	CTG	CAG	GCA	GCC	CGC	GAC	ATG	GTG	ACC	ACG	GCG	GGC	GTA	AGC	2918
Lys	Met	Leu	Gln	Ala	Ala	Arg	Asp	Met	Val	Thr	Thr	Ala	Gly	Val	Ser	
895					900					905					910	
AGC	TCC	CTG	GAC	CGC	GCC	ACT	CGC	ACC	ATC	GAG	AAT	TGG	GGT	GGC	GGC	2966
Ser	Ser	Leu	Asp	Arg	Ala	Thr	Arg	Thr	Ile	Glu	Asn	Trp	Gly	Gly	Gly	
				915					920					925		
CGC	CGT	GCG	CCC	CCA	CCG	TCC	CCC	TGC	CCG	ACC	CCG	CGG	TCT	GGC	CCC	3014
Arg	Arg	Ala	Pro	Pro	Pro	Ser	Pro	Cys	Pro	Thr	Pro	Arg	Ser	Gly	Pro	
			930					935					940			
AGC	CCA	TGC	CTG	CCC	ACC	CCC	GAC	CCG	CCC	CCA	GAG	CCG	AGC	CCC	ACG	3062
Ser	Pro	Cys	Leu	Pro	Thr	Pro	Asp	Pro	Pro	Pro	Glu	Pro	Ser	Pro	Thr	
		945					950					955				
GGC	TGG	GGA	CCG	CCA	GAC	GGG	GGT	CGC	GCG	GCG	CTT	GTG	CGC	AGG	GCT	3110
Gly	Trp	Gly	Pro	Pro	Asp	Gly	Gly	Arg	Ala	Ala	Leu	Val	Arg	Arg	Ala	
	960					965					970					
CCG	CAG	CCC	CCG	GGC	CGC	CCC	CCG	ACG	CCG	GGG	CCG	CCC	CTG	TCC	GAC	3158
Pro	Gln	Pro	Pro	Gly	Arg	Pro	Pro	Thr	Pro	Gly	Pro	Pro	Leu	Ser	Asp	
975					980					985					990	
GTC	TCC	CGA	GTG	TCG	CGC	CGC	CCA	GCC	TGG	GAG	GCG	CGG	TGG	CCG	GTG	3206
Val	Ser	Arg	Val	Ser	Arg	Arg	Pro	Ala	Trp	Glu	Ala	Arg	Trp	Pro	Val	
				995					1000					1005		
CGG	ACC	GGG	CAC	TGC	GGG	AGG	CAC	CTC	TCG	GCC	TCC	GAG	CGG	CCC	CTG	3254
Arg	Thr	Gly	His	Cys	Gly	Arg	His	Leu	Ser	Ala	Ser	Glu	Arg	Pro	Leu	
			1010					1015					1020			

10007747-120001

TCG CCC GCG CGC TGT CAC TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC	3302
Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser	
1025 1030 1035	
GGC CGC CCC TTC CTC CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC	3350
Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp	
1040 1045 1050	
CTG CCG CTG CTC GGT CCG GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG	3398
Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu	
1055 1060 1065 1070	
CAC GCG GCC TGG GCC CGG GGC TCG CGC CCG CGT CAC GCT TCC CTG CCC	3446
His Ala Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu Pro	
1075 1080 1085	
AGC TCC GTG GCC GAG GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG	3494
Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly	
1090 1095 1100	
TGC ACC GGC CCC GCC TGC GCC CGC CCC GAC GGA CAC TCG GCC TGC AGG	3542
Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg	
1105 1110 1115	
CGC TTG GCG CAG GCG CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC	3590
Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala	
1120 1125 1130	
TGC CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG	3638
Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln	
1135 1140 1145 1150	
CAC GTC TGC CTG CAC GCC CAC GCC CAC CTG CCA TTT TGC TGG GGG GCT	3686
His Val Cys Leu His Ala His Ala His Leu Pro Phe Cys Trp Gly Ala	
1155 1160 1165	
GTC TGT CCT CAC CTT CCA CCC TGT GCC AGC CAC GGC TCC TGG CTC TCC	3734
Val Cys Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu Ser	
1170 1175 1180	
GGG GCC TGG GGG CCT CTG GGG CAC AGG GGC AGG ACT CTG GGG CTG GGC	3782
Gly Ala Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu Gly	
1185 1190 1195	
ACA GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC AGG GTA GCC	3830
Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Arg Val Ala	
1200 1205 1210	
CGT GGG ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC	3878
Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser	
1215 1220 1225 1230	
AGT CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA	3926
Ser Leu Glu Ser Glu Val	
1235	
GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG GCTTTTCTGG	3986
CTTCTACCAT GAAATCCTGG CCATGGGACC CCAGTGACAG ATGATGTCTT CCATGGTCAT	4046
CAGTGACCTC AGTAGCCTCA AATCATGGTG AGGGCTGGGC TTTGCTGTC CTCTTCTCAC	4106
GCAGAGTTCT GCCAGGAGGG TGTGCTGTGG GGGTCAGACT CCTGAGGCTC TCCCTTCCCT	4166
GGGGCTAGCC AGTTACTGGT CATGCCTGCT GTGGGCATGG AGGCTGGAAC TTGTGGTTGA	4226

T00074701

GGCAGGGCCA TCCCGATCCT TGCTCTACCT GGCTAGAGTT TCTTCTCATC AGAGCACTGG 4286
 GACATTAAAC CCACCTTTTC CCAGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAG 4340

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly
 1 5 10 15
 Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val
 20 25 30
 Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val
 35 40 45
 Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro
 50 55 60
 Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln
 65 70 75 80
 Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu
 85 90 95
 Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser
 100 105 110
 Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val
 115 120 125
 Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val
 130 135 140
 Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr
 145 150 155 160
 Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala
 165 170 175
 Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser
 180 185 190
 Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro
 195 200 205
 Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe
 210 215 220
 Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala
 225 230 235 240
 Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn
 245 250 255
 Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly
 260 265 270

1000747 120701

Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys
 275 280 285
 Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp
 290 295 300
 Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His
 305 310 315 320
 Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu
 325 330 335
 Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr
 340 345 350
 Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu
 355 360 365
 Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr
 370 375 380
 Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser
 385 390 395 400
 Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val
 405 410 415
 Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro
 420 425 430
 Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro
 435 440 445
 Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys
 450 455 460
 Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn
 465 470 475 480
 Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly
 485 490 495
 Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile
 500 505 510
 Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu
 515 520 525
 Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro
 530 535 540
 Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe
 545 550 555 560
 Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr
 565 570 575
 Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Lys Ser
 580 585 590
 Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala
 595 600 605
 Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr
 610 615 620

10007747-10001
 10007747-10001

Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu
 625 630 635 640
 Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr
 645 650 655
 Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln
 660 665 670
 Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr
 675 680 685
 Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val
 690 695 700
 Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met
 705 710 715 720
 Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Val Leu Asn Tyr Met
 725 730 735
 Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys
 740 745 750
 Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His
 755 760 765
 Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly
 770 775 780
 Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn
 785 790 795 800
 Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala
 805 810 815
 Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val
 820 825 830
 Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro
 835 840 845
 Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr
 850 855 860
 Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala
 865 870 875 880
 Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Met
 885 890 895
 Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Ser Ser
 900 905 910
 Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Gly Arg Arg
 915 920 925
 Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro
 930 935 940
 Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp
 945 950 955 960
 Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln
 965 970 975

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Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser
 980 985 990
 Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr
 995 1000 1005
 Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro
 1010 1015 1020
 Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg
 1025 1030 1035 1040
 Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro
 1045 1050 1055
 Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu His Ala
 1060 1065 1070
 Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu Pro Ser Ser
 1075 1080 1085
 Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr
 1090 1095 1100
 Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu
 1105 1110 1115 1120
 Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln
 1125 1130 1135
 Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val
 1140 1145 1150
 Cys Leu His Ala His Ala His Leu Pro Phe Cys Trp Gly Ala Val Cys
 1155 1160 1165
 Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu Ser Gly Ala
 1170 1175 1180
 Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu Gly Thr Gly
 1185 1190 1195 1200
 Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Arg Val Ala Arg Gly
 1205 1210 1215
 Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu
 1220 1225 1230
 Glu Ser Glu Val
 1235

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..22

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

C TCT GAG GCT CAG CCT GTC CCC AG
Ser Glu Ala Gln Pro Val Pro
1 5

24

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Glu Ala Gln Pro Val Pro
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGAAGGGGGT G

11

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4808 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 311..4705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCATGGGAC CGGGTGAGCG CTGAGAATCG CGGCCGACG CATCAGCCCT GGAGATGACC	60
AGGAGCGGCC ACTGCTGAGA ACTATGTGGA GAGAGGCTGC GAGCCCTGCT GCAGAGCCTC	120
CGGCTGGGAT AGCCGCCCCC CGTGGGGGCG ATGCGGACAG CGCGGGACAG CCAGGGGAGC	180
GCGCTGGGGC CGCAGCATGC GGGAACCCGC TAAACCCGGT GGCTGCTGAG GCGGCCGAGA	240
TGCTCGTGCG CGCAGCGCGC CCCACTGCAT CCTCGACCTT CTCGGGCTAC AGGGACCGTC	300

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AGTGGCGACT	ATG	GGC	AGA	GTG	GGC	TAT	TGG	ACC	CTG	CTG	GTG	CTG	CCG			349
	Met	Gly	Arg	Val	Gly	Tyr	Trp	Thr	Leu	Leu	Val	Leu	Pro			
	1				5					10						
GCC CTT CTG GTC TGG CGC GGT CCG GCG CCG AGC GCG GCG GCG GAG AAG																397
Ala Leu Leu Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys																
	15					20				25						
GGT CCC CCC GCG CTA AAT ATT GCG GTG ATG CTG GGT CAC AGC CAC GAC																445
Gly Pro Pro Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp																
	30				35				40						45	
GTG ACA GAG CGC GAA CTT CGA ACA CTG TGG GGC CCC GAG CAG GCG GCG																493
Val Thr Glu Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala																
				50				55						60		
GGG CTG CCC CTG GAC GTG AAC GTG GTA GCT CTG CTG ATG AAC CGC ACC																541
Gly Leu Pro Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr																
			65				70						75			
GAC CCC AAG AGC CTC ATC ACG CAC GTG TGC GAC CTC ATG TCC GGG GCA																589
Asp Pro Lys Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala																
		80					85					90				
CGC ATC CAC GGC CTC GTG TTT GGG GAC GAC ACG GAC CAG GAG GCC GTA																637
Arg Ile His Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val																
	95					100					105					
GCC CAG ATG CTG GAT TTT ATC TCC TCC CAC ACC TTC GTC CCC ATC TTG																685
Ala Gln Met Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu																
	110				115				120						125	
GGC ATT CAT GGG GGC GCA TCT ATG ATC ATG GCT GAC AAG GAT CCG ACG																733
Gly Ile His Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr																
			130				135						140			
TCT ACC TTC TTC CAG TTT GGA GCG TCC ATC CAG CAG CAA GCC ACG GTC																781
Ser Thr Phe Phe Gln Phe Gly Ala Ser Ile Gln Gln Gln Ala Thr Val																
			145				150						155			
ATG CTG AAG ATC ATG CAG GAT TAT GAC TGG CAT GTC TTC TCC CTG GTG																829
Met Leu Lys Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val																
		160					165					170				
ACC ACT ATC TTC CCT GGC TAC AGG GAA TTC ATC AGC TTC GTC AAG ACC																877
Thr Thr Ile Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr																
		175				180					185					
ACA GTG GAC AAC AGC TTT GTG GGC TGG GAC ATG CAG AAT GTG ATC ACA																925
Thr Val Asp Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr																
	190				195				200						205	
CTG GAC ACT TCC TTT GAG GAT GCA AAG ACA CAA GTC CAG CTG AAG AAG																973
Leu Asp Thr Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys																
			210				215						220			
ATC CAC TCT TCT GTC ATC TTG CTC TAC TGT TCC AAA GAC GAG GCT GTT																1021
Ile His Ser Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val																
			225				230						235			
CTC ATT CTG AGT GAG GCC CGC TCC CTT GGC CTC ACC GGG TAT GAT TTC																1069
Leu Ile Leu Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe																
		240				245						250				
TTC TGG ATT GTC CCC AGC TTG GTC TCT GGG AAC ACG GAG CTC ATC CCA																1117
Phe Trp Ile Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro																
	255				260				265							

AAA	GAG	TTT	CCA	TCG	GGA	CTC	ATT	TCT	GTC	TCC	TAC	GAT	GAC	TGG	GAC	1165
Lys	Glu	Phe	Pro	Ser	Gly	Leu	Ile	Ser	Val	Ser	Tyr	Asp	Asp	Trp	Asp	
270					275					280					285	
TAC	AGC	CTG	GAG	GGG	AGA	GTG	AGG	GAC	GGC	ATT	GGC	ATC	CTA	ACC	ACC	1213
Tyr	Ser	Leu	Glu	Ala	Arg	Val	Arg	Asp	Gly	Ile	Gly	Ile	Leu	Thr	Thr	
				290					295					300		
GCT	GCA	TCT	TCT	ATG	CTG	GAG	AAG	TTC	TCC	TAC	ATC	CCC	GAG	GCC	AAG	1261
Ala	Ala	Ser		Met	Leu	Glu	Lys	Phe	Ser	Tyr	Ile	Pro	Glu	Ala	Lys	
			305					310					315			
GCC	AGC	TGC	TAC	GGG	CAG	ATG	GAG	AGG	CCA	GAG	GTC	CCG	ATG	CAC	ACC	1309
Ala	Ser	Cys	Tyr	Gly	Gln	Met	Glu	Arg	Pro	Glu	Val		Pro	Met	His	
		320					325					330			Thr	
TTG	CAC	CCA	TTT	ATG	GTC	AAT	GTT	ACA	TGG	GAT	GGC	AAA	GAC	TTA	TCC	1357
Leu	His	Pro	Phe	Met	Val	Asn	Val	Thr	Trp	Asp	Gly	Lys	Asp	Leu	Ser	
	335					340					345					
TTC	ACT	GAG	GAA	GGC	TAC	CAG	GTG	CAC	CCC	AGG	CTG	GTG	GTG	ATT	GTG	1405
Phe	Thr	Glu	Glu	Gly	Tyr	Gln	Val	His	Pro	Arg	Leu	Val	Val	Ile	Val	
350					355					360					365	
CTG	AAC	AAA	GAC	CGG	GAA	TGG	GAA	AAG	GTG	GGC	AAG	TGG	GAG	AAC	CAT	1453
Leu	Asn	Lys	Asp	Arg	Glu	Trp	Glu	Lys	Val	Gly	Lys	Trp	Glu	Asn	His	
				370					375					380		
ACG	CTG	AGC	CTG	AGG	CAC	GCC	GTG	TGG	CCC	AGG	TAC	AAG	TCC	TTC	TCC	1501
Thr	Leu	Ser	Leu	Arg	His	Ala	Val	Trp	Pro	Arg	Tyr	Lys	Ser	Phe	Ser	
			385					390					395			
GAC	TGT	GAG	CCG	GAT	GAC	AAC	CAT	CTC	AGC	ATC	GTC	ACC	CTG	GAG	GAG	1549
Asp	Cys	Glu	Pro	Asp	Asp	Asn	His	Leu	Ser	Ile	Val	Thr	Leu	Glu	Glu	
		400					405					410				
GCC	CCA	TTC	GTC	ATC	GTG	GAA	GAC	ATA	GAC	CCC	CTG	ACC	GAG	ACG	TGT	1597
Ala	Pro	Phe	Val	Ile	Val	Glu	Asp	Ile	Asp	Pro	Leu	Thr	Glu	Thr	Cys	
	415					420					425					
GTG	AGG	AAC	ACC	GTG	CCA	TGT	CGG	AAG	TTC	GTC	AAA	ATC	AAC	AAT	TCA	1645
Val	Arg	Asn	Thr	Val	Pro	Cys	Arg	Lys	Phe	Val	Lys	Ile	Asn	Asn	Ser	
430					435					440					445	
ACC	AAT	GAG	GGG	ATG	AAT	GTG	AAG	AAA	TGC	TGC	AAG	GGG	TTC	TGC	ATT	1693
Thr	Asn	Glu	Gly	Met	Asn	Val	Lys	Lys	Cys	Cys	Lys	Gly	Phe	Cys	Ile	
				450					455					460		
GAT	ATT	CTG	AAG	AAG	CTT	TCC	AGA	ACT	GTG	AAG	TTT	ACT	TAC	GAC	CTC	1741
Asp	Ile	Leu	Lys	Lys	Leu	Ser	Arg	Thr	Val	Lys	Phe	Thr	Tyr	Asp	Leu	
			465					470					475			
TAT	CTG	GTG	ACC	AAT	GGG	AAG	CAT	GGC	AAG	AAA	GTT	AAC	AAT	GTG	TGG	1789
Tyr	Leu	Val	Thr	Asn	Gly	Lys	His	Gly	Lys	Lys	Val	Asn	Asn	Val	Trp	
		480					485					490				
AAT	GGA	ATG	ATC	GGT	GAA	GTG	GTC	TAT	CAA	CGG	GCA	GTC	ATG	GCA	GTT	1837
Asn	Gly	Met	Ile	Gly	Glu	Val	Val	Tyr	Gln	Arg	Ala	Val	Met	Ala	Val	
	495					500					505					
GGC	TCG	CTC	ACC	ATC	AAT	GAG	GAA	CGT	TCT	GAA	GTG	GTG	GAC	TTC	TCT	1885
Gly	Ser	Leu	Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Val	Val	Asp	Phe	Ser	
510					515					520					525	
GTG	CCC	TTT	GTG	GAA	ACG	GGA	ATC	AGT	GTC	ATG	GTT	TCA	AGA	AGT	AAT	1933
Val	Pro	Phe	Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ser	Arg	Ser	Asn	
				530					535					540		

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GGC ACC GTC TCA CCT TCT GCT TTT CTA GAA CCA TTC AGC GCC TCT GTC	1981
Gly Thr Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val	
545 550 555	
TGG GTG ATG ATG TTT GTG ATG CTG CTC ATT GTT TCT GCC ATA GCT GTT	2029
Trp Val Met Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val	
560 565 570	
TGG GTC TTG GAT TAC TCC AGC CCT GTT GGA TAC AAC AGA AAC TTA GCC	2077
Trp Val Leu Asp Tyr Ser Ser Pro Val Gly Tyr Asn Arg Asn Leu Ala	
575 580 585	
AAA GGG AAA GCA CCC CAT GGG CCT TCT TTT ACA ATT GGA AAA GCT ATA	2125
Lys Gly Lys Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile	
590 595 600 605	
TGG CTT CTT TGG GGC CTG GTG TTC AAT AAC TCC GTG CCT GTC CAG AAT	2173
Trp Leu Leu Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn	
610 615 620	
CCT AAA GGG ACC ACC AGC AAG ATC ATG GTA TCT GTA TGG GCC TTC TTC	2221
Pro Lys Gly Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe	
625 630 635	
GCT GTC ATA TTC CTG GCT AGC TAC ACA GCC AAT CTG GCT GCC TTC ATG	2269
Ala Val Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met	
640 645 650	
ATC CAA GAG GAA TTT GTG GAC CAA GTG ACC GGC CTC AGT GAC AAA AAG	2317
Ile Gln Glu Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys	
655 660 665	
TTT CAG AGA CCT CAT GAC TAT TCC CCA CCT TTT CGA TTT GGG ACA GTG	2365
Phe Gln Arg Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val	
670 675 680 685	
CCT AAT GGA AGC ACG GAG AGA AAC ATT CGG AAT AAC TAT CCC TAC ATG	2413
Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met	
690 695 700	
CAT CAG TAC ATG ACC AAA TTT AAT CAG AAA GGA GTA GAG GAC GCC TTG	2461
His Gln Tyr Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu	
705 710 715	
GTC AGC CTG AAA ACG GGG AAG CTG GAC GCT TTC ATC TAC GAT GCC GCA	2509
Val Ser Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala	
720 725 730	
GTC TTG AAT TAC AAG GCT GGG AGG GAT GAA GGC TGC AAG CTG GTG ACC	2557
Val Leu Asn Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr	
735 740 745	
ATC GGG AGT GGG TAC ATC TTT GCC ACC ACC GGT TAT GGA ATT GCC CTT	2605
Ile Gly Ser Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu	
750 755 760 765	
CAG AAA GGC TCT CCT TGG AAG AGG CAG ATC GAC CTG GCC TTG CTT CAG	2653
Gln Lys Gly Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Leu Gln	
770 775 780	
TTT GTG GGT GAT GGT GAG ATG GAG GAG CTG GAG ACC CTG TGG CTC ACT	2701
Phe Val Gly Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr	
785 790 795	
GGG ATC TGC CAC AAC GAG AAG AAC GAG GTG ATG AGC AGC CAG CTG GAC	2749
Gly Ile Cys His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp	
800 805 810	

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ATT	GAC	AAC	ATG	GCG	GGC	GTA	TTC	TAC	ATG	CTG	GCT	GCC	GCC	ATG	GCC	2797
Ile	Asp	Asn	Met	Ala	Gly	Val	Phe	Tyr	Met	Leu	Ala	Ala	Ala	Met	Ala	
815						820					825					
CTT	AGC	CTC	ATC	ACC	TTC	ATC	TGG	GAG	CAC	CTC	TTC	TAC	TGG	AAG	CTG	2845
Leu	Ser	Leu	Ile	Thr	Phe	Ile	Trp	Glu	His	Leu	Phe	Tyr	Trp	Lys	Leu	
830					835					840					845	
CGC	TTC	TGT	TTC	ACG	GGC	GTG	TGC	TCC	GAC	CGG	CCT	GGG	TTG	CTC	TTC	2893
Arg	Phe	Cys	Phe	Thr	Gly	Val	Cys	Ser	Asp	Arg	Pro	Gly	Leu	Leu	Phe	
				850					855					860		
TCC	ATC	AGC	AGG	GGC	ATC	TAC	AGC	TGC	ATT	CAT	GGA	GTG	CAC	ATT	GAA	2941
Ser	Ile	Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Ile	His	Gly	Val	His	Ile	Glu	
			865					870					875			
GAA	AAG	AAG	AAG	TCT	CCA	GAC	TTC	AAT	CTG	ACG	GGA	TCC	CAG	AGC	AAC	2989
Glu	Lys	Lys	Lys	Ser	Pro	Asp	Phe	Asn	Leu	Thr	Gly	Ser	Gln	Ser	Asn	
		880				885						890				
ATG	TTA	AAA	CTC	CTC	CGG	TCA	GCC	AAA	AAC	ATT	TCC	AGC	ATG	TCC	AAC	3037
Met	Leu	Lys	Leu	Leu	Arg	Ser	Ala	Lys	Asn	Ile	Ser	Ser	Met	Ser	Asn	
	895					900					905					
ATG	AAC	TCC	TCA	AGA	ATG	GAC	TCA	CCC	AAA	AGA	GCT	GCT	GAC	TTC	ATC	3085
Met	Asn	Ser	Ser	Arg	Met	Asp	Ser	Pro	Lys	Arg	Ala	Ala	Asp	Phe	Ile	
910					915					920					925	
CAA	AGA	GGT	TCC	CTC	ATC	ATG	GAC	ATG	GTT	TCA	GAT	AAG	GGG	AAT	TTG	3133
Gln	Arg	Gly	Ser	Leu	Ile	Met	Asp	Met	Val	Ser	Asp	Lys	Gly	Asn	Leu	
				930					935					940		
ATG	TAC	TCA	GAC	AAC	AGG	TCC	TTT	CAG	GGG	AAA	GAG	AGC	ATT	TTT	GGA	3181
Met	Tyr	Ser	Asp	Asn	Arg	Ser	Phe	Gln	Gly	Lys	Glu	Ser	Ile	Phe	Gly	
			945					950					955			
GAC	AAC	ATG	AAC	GAA	CTC	CAA	ACA	TTT	GTG	GCC	AAC	CGG	CAG	AAG	GAT	3229
Asp	Asn	Met	Asn	Glu	Leu	Gln	Thr	Phe	Val	Ala	Asn	Arg	Gln	Lys	Asp	
		960					965					970				
AAC	CTC	AAT	AAC	TAT	GTA	TTC	CAG	GGA	CAA	CAT	CCT	CTT	ACT	CTC	AAT	3277
Asn	Leu	Asn	Asn	Tyr	Val	Phe	Gln	Gly	Gln	His	Pro	Leu	Thr	Leu	Asn	
	975					980					985					
GAG	TCC	AAC	CCT	AAC	ACG	GTG	GAG	GTG	GCC	GTG	AGC	ACA	GAA	TCC	AAA	3325
Glu	Ser	Asn	Pro	Asn	Thr	Val	Glu	Val	Ala	Val	Ser	Thr	Glu	Ser	Lys	
990					995				1000						1005	
GCG	AAC	TCT	AGA	CCC	CGG	CAG	CTG	TGG	AAG	AAA	TCC	GTG	GAT	TCC	ATA	3373
Ala	Asn	Ser	Arg	Pro	Arg	Gln	Leu	Trp	Lys	Lys	Ser	Val	Asp	Ser	Ile	
				1010					1015					1020		
CGC	CAG	GAT	TCA	CTA	TCC	CAG	AAT	CCA	GTC	TCC	CAG	AGG	GAT	GAG	GCA	3421
Arg	Gln	Asp	Ser	Leu	Ser	Gln	Asn	Pro	Val	Ser	Gln	Arg	Asp	Glu	Ala	
			1025					1030					1035			
ACA	GCA	GAG	AAT	AGG	ACC	CAC	TCC	CTA	AAG	AGC	CCT	AGG	TAT	CTT	CCA	3469
Thr	Ala	Glu	Asn	Arg	Thr	His	Ser	Leu	Lys	Ser	Pro	Arg	Tyr	Leu	Pro	
		1040					1045					1050				
GAA	GAG	ATG	GCC	CAC	TCT	GAC	ATT	TCA	GAA	ACG	TCA	AAT	CGG	GCC	ACG	3517
Glu	Glu	Met	Ala	His	Ser	Asp	Ile	Ser	Glu	Thr	Ser	Asn	Arg	Ala	Thr	
		1055				1060					1065					
TGC	CAC	AGG	GAA	CCT	GAC	AAC	AGT	AAG	AAC	CAC	AAA	ACC	AAG	GAC	AAC	3565
Cys	His	Arg	Glu	Pro	Asp	Asn	Ser	Lys	Asn	His	Lys	Thr	Lys	Asp	Asn	
1070						1075				1080					1085	

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TTT AAA AGG TCA GTG GCC TCC AAA TAC CCC AAG GAC TGT AGT GAG GTC Phe Lys Arg Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val 1090 1095 1100	3613
GAG CGC ACC TAC CTG AAA ACC AAA TCA AGC TCC CCT AGA GAC AAG ATC Glu Arg Thr Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile 1105 1110 1115	3661
TAC ACT ATA GAT GGT GAG AAG GAG CCT GGT TTC CAC TTA GAT CCA CCC Tyr Thr Ile Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro 1120 1125 1130	3709
CAG TTT GTT GAA AAT GTG ACC CTG CCC GAG AAC GTG GAC TTC CCG GAC Gln Phe Val Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp 1135 1140 1145	3757
CCC TAC CAG GAT CCC AGT GAA AAC TTC CGC AAG GGG GAC TCC ACG CTG Pro Tyr Gln Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu 1150 1155 1160 1165	3805
CCA ATG AAC CGG AAC CCC TTG CAT AAT GAA GAG GGG CTT TCC AAC AAC Pro Met Asn Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn 1170 1175 1180	3853
GAC CAG TAT AAA CTC TAC TCC AAG CAC TTC ACC TTG AAA GAC AAG GGT Asp Gln Tyr Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly 1185 1190 1195	3901
TCC CCG CAC AGT GAG ACC AGC GAG CGA TAC CGG CAG AAC TCC ACG CAC Ser Pro His Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His 1200 1205 1210	3949
TGC AGA AGC TGC CTT TCC AAC ATG CCC ACC TAT TCA GGC CAC TTC ACC Cys Arg Ser Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr 1215 1220 1225	3997
ATG AGG TCC CCC TTC AAG TGC GAT GCC TGC CTG CGG ATG GGG AAC CTC Met Arg Ser Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu 1230 1235 1240 1245	4045
TAT GAC ATC GAT GAA GAC CAG ATG CTT CAG GAG ACA GGT AAC CCA GCC Tyr Asp Ile Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala 1250 1255 1260	4093
ACC GGG GAG CAG GTC TAC CAG CAG GAC TGG GCA CAG AAC AAT GCC CTT Thr Gly Glu Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu 1265 1270 1275	4141
CAA TTA CAA AAG AAC AAG CTA AGG ATT AGC CGT CAG CAT TCC TAC GAT Gln Leu Gln Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp 1280 1285 1290	4189
AAC ATT GTC GAC AAA CCT AGG GAG CTA GAC CTT AGC AGG CCC TCC CGG Asn Ile Val Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg 1295 1300 1305	4237
AGC ATA AGC CTC AAG GAC AGG GAA CGG CTT CTG GAG GGA AAT TTT TAC Ser Ile Ser Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr 1310 1315 1320 1325	4285
GGC AGC CTG TTT AGT GTC CCC TCA AGC AAA CTC TCG GGG AAA AAA AGC Gly Ser Leu Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser 1330 1335 1340	4333
TCC CTT TTC CCC CAA GGT CTG GAG GAC AGC AAG AGG AGC AAG TCT CTC Ser Leu Phe Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu 1345 1350 1355	4381

T0202T 440001

TTG CCA GAC CAC ACC TCC GAT AAC CCT TTC CTC CAC TCC CAC AGG GAT	4429
Leu Pro Asp His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp	
1360 1365 1370	
GAC CAA CGC TTG GTT ATT GGG AGA TGC CCC TCG GAC CCT TAC AAA CAC	4477
Asp Gln Arg Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His	
1375 1380 1385	
TCG TTG CCA TCC CAG GCG GTG AAT GAC AGC TAT CTT CGG TCG TCC TTG	4525
Ser Leu Pro Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu	
1390 1395 1400 1405	
AGG TCA ACG GCA TCG TAC TGT TCC AGG GAC AGT CGG GGC CAC AAT GAT	4573
Arg Ser Thr Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp	
1410 1415 1420	
GTG TAT ATT TCG GAG CAT GTT ATG CCT TAT GCT GCA AAT AAG AAT AAT	4621
Val Tyr Ile Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn	
1425 1430 1435	
ATG TAC TCT ACC CCC AGG GTT TTA AAT TCC TGC AGC AAT AGA CGC GTG	4669
Met Tyr Ser Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val	
1440 1445 1450	
TAC AAG GAA ATG CCT AGT ATC GAA TCT GAT GTT TAAAAATCTT CCATTAATGT	4722
Tyr Lys Glu Met Pro Ser Ile Glu Ser Asp Val	
1455 1460 146	
TTTATCTATA GGGAAATACA CGTAATGGCC AATGTTCTGG AGGGTAAATG TTGGATGTCC	4782
AATAGTGCCC TGCTAAGAGG AAGGAG	4808

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1464 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro Ala Leu Leu	
1 5 10 15	
Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys Gly Pro Pro	
20 25 30	
Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp Val Thr Glu	
35 40 45	
Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala Gly Leu Pro	
50 55 60	
Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr Asp Pro Lys	
65 70 75 80	
Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala Arg Ile His	
85 90 95	
Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val Ala Gln Met	
100 105 110	
Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu Gly Ile His	
115 120 125	

T000274-120001

Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr Ser Thr Phe
 130 135 140
 Phe Gln Phe Gly Ala Ser Ile Gln Gln Gln Ala Thr Val Met Leu Lys
 145 150 155 160
 Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val Thr Thr Ile
 165 170 175
 Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr Thr Val Asp
 180 185 190
 Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr Leu Asp Thr
 195 200 205
 Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys Ile His Ser
 210 215 220
 Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val Leu Ile Leu
 225 230 235 240
 Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe Phe Trp Ile
 245 250 255
 Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro Lys Glu Phe
 260 265 270
 Pro Ser Gly Leu Ile Ser Val Ser Tyr Asp Asp Trp Asp Tyr Ser Leu
 275 280 285
 Glu Ala Arg Val Arg Asp Gly Ile Gly Ile Leu Thr Thr Ala Ala Ser
 290 295 300
 Ser Met Leu Glu Lys Phe Ser Tyr Ile Pro Glu Ala Lys Ala Ser Cys
 305 310 315 320
 Tyr Gly Gln Met Glu Arg Pro Glu Val Pro Met His Thr Leu His Pro
 325 330 335
 Phe Met Val Asn Val Thr Trp Asp Gly Lys Asp Leu Ser Phe Thr Glu
 340 345 350
 Glu Gly Tyr Gln Val His Pro Arg Leu Val Val Ile Val Leu Asn Lys
 355 360 365
 Asp Arg Glu Trp Glu Lys Val Gly Lys Trp Glu Asn His Thr Leu Ser
 370 375 380
 Leu Arg His Ala Val Trp Pro Arg Tyr Lys Ser Phe Ser Asp Cys Glu
 385 390 395 400
 Pro Asp Asp Asn His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe
 405 410 415
 Val Ile Val Glu Asp Ile Asp Pro Leu Thr Glu Thr Cys Val Arg Asn
 420 425 430
 Thr Val Pro Cys Arg Lys Phe Val Lys Ile Asn Asn Ser Thr Asn Glu
 435 440 445
 Gly Met Asn Val Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu
 450 455 460
 Lys Lys Leu Ser Arg Thr Val Lys Phe Thr Tyr Asp Leu Tyr Leu Val
 465 470 475 480

1000744-12001
 1000744-12001

Thr Asn Gly Lys His Gly Lys Lys Val Asn Asn Val Trp Asn Gly Met
 485 490 495
 Ile Gly Glu Val Val Tyr Gln Arg Ala Val Met Ala Val Gly Ser Leu
 500 505 510
 Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro Phe
 515 520 525
 Val Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr Val
 530 535 540
 Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val Trp Val Met
 545 550 555 560
 Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val Trp Val Leu
 565 570 575
 Asp Tyr Ser Ser Pro Val Gly Tyr Asn Arg Asn Leu Ala Lys Gly Lys
 580 585 590
 Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu Leu
 595 600 605
 Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys Gly
 610 615 620
 Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val Ile
 625 630 635 640
 Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu
 645 650 655
 Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys Phe Gln Arg
 660 665 670
 Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly
 675 680 685
 Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met His Gln Tyr
 690 695 700
 Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu Val Ser Leu
 705 710 715 720
 Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn
 725 730 735
 Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser
 740 745 750
 Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu Gln Lys Gly
 755 760 765
 Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Leu Gln Phe Val Gly
 770 775 780
 Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr Gly Ile Cys
 785 790 795 800
 His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp Asn
 805 810 815
 Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala Leu Ser Leu
 820 825 830

10007747-120701

Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu Arg Phe Cys
 835 840 845
 Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe Ser Ile Ser
 850 855 860
 Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu Glu Lys Lys
 865 870 875 880
 Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn Met Leu Lys
 885 890 895
 Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn Met Asn Ser
 900 905 910
 Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile Gln Arg Gly
 915 920 925
 Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu Met Tyr Ser
 930 935 940
 Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly Asp Asn Met
 945 950 955 960
 Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp Asn Leu Asn
 965 970 975
 Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn Glu Ser Asn
 980 985 990
 Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys Ala Asn Ser
 995 1000 1005
 Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile Arg Gln Asp
 1010 1015 1020
 Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala Thr Ala Glu
 1025 1030 1035 1040
 Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro Glu Glu Met
 1045 1050 1055
 Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr Cys His Arg
 1060 1065 1070
 Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn Phe Lys Arg
 1075 1080 1085
 Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val Glu Arg Thr
 1090 1095 1100
 Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile Tyr Thr Ile
 1105 1110 1115 1120
 Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro Gln Phe Val
 1125 1130 1135
 Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp Pro Tyr Gln
 1140 1145 1150
 Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu Pro Met Asn
 1155 1160 1165
 Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn Asp Gln Tyr
 1170 1175 1180

1000747-120701
 1000747-120701

Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly Ser Pro His
 1185 1190 1195 1200
 Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His Cys Arg Ser
 1205 1210 1215
 Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr Met Arg Ser
 1220 1225 1230
 Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu Tyr Asp Ile
 1235 1240 1245
 Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala Thr Gly Glu
 1250 1255 1260
 Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu Gln Leu Gln
 1265 1270 1275 1280
 Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp Asn Ile Val
 1285 1290 1295
 Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg Ser Ile Ser
 1300 1305 1310
 Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr Gly Ser Leu
 1315 1320 1325
 Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser Ser Leu Phe
 1330 1335 1340
 Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu Leu Pro Asp
 1345 1350 1355 1360
 His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp Asp Gln Arg
 1365 1370 1375
 Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His Ser Leu Pro
 1380 1385 1390
 Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu Arg Ser Thr
 1395 1400 1405
 Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp Val Tyr Ile
 1410 1415 1420
 Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn Met Tyr Ser
 1425 1430 1435 1440
 Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val Tyr Lys Glu
 1445 1450 1455
 Met Pro Ser Ile Glu Ser Asp Val
 1460

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

F0402T-4420001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAGGGAGGC GGCCGGCGCG GACTCTCTTC GCGGGCGCAG CGCCCCTTCC CCCTCGGACC 60
CTCCGGTGGA CATG 74

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 210..4664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTGAATTTGC ATCTCTTCAA GACACAAGAT TAAACAAAA TTTACGCTAA ATTGGATTTT 60
AAATTATCTT CCGTTCATTT ATCCTTCGTC TTTCTTATGT GGATATGCAA GCGAGAAGAA 120
GGGACTGGAC ATTCCAACA TGCTCACTCC CTTAATCTGT CCGTCTAGAG GTTTGGCTTC 180
TACAAACCAA GGGAGTCGAC GAGTTGAAG ATG AAG CCC AGA GCG GAG TGC TGT 233
Met Lys Pro Arg Ala Glu Cys Cys
1 5
TCT CCC AAG TTC TGG TTG GTG TTG GCC GTC CTG GCC GTG TCA GGC AGC 281
Ser Pro Lys Phe Trp Leu Val Leu Ala Val Leu Ala Val Ser Gly Ser
10 15 20
AGA GCT CGT TCT CAG AAG AGC CCC CCC AGC ATT GGC ATT GCT GTC ATC 329
Arg Ala Arg Ser Gln Lys Ser Pro Pro Ser Ile Gly Ile Ala Val Ile
25 30 35 40
CTC GTG GGC ACT TCC GAC GAG GTG GCC ATC AAG GAT GCC CAC GAG AAA 377
Leu Val Gly Thr Ser Asp Glu Val Ala Ile Lys Asp Ala His Glu Lys
45 50 55
GAT GAT TTC CAC CAT CTC TCC GTG GTA CCC CGG GTG GAA CTG GTA GCC 425
Asp Asp Phe His His Leu Ser Val Val Pro Arg Val Glu Leu Val Ala
60 65 70
ATG AAT GAG ACC GAC CCA AAG AGC ATC ATC ACC CGC ATC TGT GAT CTC 473
Met Asn Glu Thr Asp Pro Lys Ser Ile Ile Thr Arg Ile Cys Asp Leu
75 80 85
ATG TCT GAC CGG AAG ATC CAG GGG GTG GTG TTT GCT GAT GAC ACA GAC 521
Met Ser Asp Arg Lys Ile Gln Gly Val Val Phe Ala Asp Asp Thr Asp
90 95 100
CAG GAA GCC ATC GCC CAG ATC CTC GAT TTC ATT TCA GCA CAG ACT CTC 569
Gln Glu Ala Ile Ala Gln Ile Leu Asp Phe Ile Ser Ala Gln Thr Leu
105 110 115 120
ACC CCG ATC CTG GGC ATC CAC GGG GGC TCC TCT ATG ATA ATG GCA GAT 617
Thr Pro Ile Leu Gly Ile His Gly Gly Ser Ser Met Ile Met Ala Asp
125 130 135

10007747-120701

AAG	GAT	GAA	TCC	TCC	ATG	TTC	TTC	CAG	TTT	GGC	CCA	TCA	ATT	GAA	CAG	665
Lys	Asp	Glu	Ser	Ser	Met	Phe	Phe	Gln	Phe	Gly	Pro	Ser	Ile	Glu	Gln	
			140					145					150			
CAA	GCT	TCC	GTA	ATG	CTC	AAC	ATC	ATG	GAA	GAA	TAT	GAC	TGG	TAC	ATC	713
Gln	Ala	Ser	Val	Met	Leu	Asn	Ile	Met	Glu	Glu	Tyr	Asp	Trp	Tyr	Ile	
		155					160					165				
TTT	TCT	ATC	GTC	ACC	ACC	TAT	TTC	CCT	GGC	TAC	CAG	GAC	TTT	GTA	AAC	761
Phe	Ser	Ile	Val	Thr	Thr	Tyr	Phe	Pro	Gly	Tyr	Gln	Asp	Phe	Val	Asn	
	170					175					180					
AAG	ATC	CGC	AGC	ACC	ATT	GAG	AAT	AGC	TTT	GTG	GGC	TGG	GAG	CTA	GAG	809
Lys	Ile	Arg	Ser	Thr	Ile	Glu	Asn	Ser	Phe	Val	Gly	Trp	Glu	Leu	Glu	
185					190					195					200	
GAG	GTC	CTC	CTA	CTG	GAC	ATG	TCC	CTG	GAC	GAT	GGA	GAT	TCT	AAG	ATC	857
Glu	Val	Leu	Leu	Leu	Asp	Met	Ser	Leu	Asp	Asp	Gly	Asp	Ser	Lys	Ile	
				205					210					215		
CAG	AAT	CAG	CTC	AAG	AAA	CTT	CAA	AGC	CCC	ATC	ATT	CTT	CTT	TAC	TGT	905
Gln	Asn	Gln	Leu	Lys	Lys	Leu	Gln	Ser	Pro	Ile	Ile	Leu	Leu	Tyr	Cys	
			220					225					230			
ACC	AAG	GAA	GAA	GCC	ACC	TAC	ATC	TTT	GAA	GTG	GCC	AAC	TCA	GTA	GGG	953
Thr	Lys	Glu	Glu	Ala	Thr	Tyr	Ile	Phe	Glu	Val	Ala	Asn	Ser	Val	Gly	
		235					240					245				
CTG	ACT	GGC	TAT	GGC	TAC	ACG	TGG	ATC	GTG	CCC	AGT	CTG	GTG	GCA	GGG	1001
Leu	Thr	Gly	Tyr	Gly	Tyr	Thr	Trp	Ile	Val	Pro	Ser	Leu	Val	Ala	Gly	
	250					255					260					
GAT	ACA	GAC	ACA	GTG	CCT	GCG	GAG	TTC	CCC	ACT	GGG	CTC	ATC	TCT	GTA	1049
Asp	Thr	Asp	Thr	Val	Pro	Ala	Glu	Phe	Pro	Thr	Gly	Leu	Ile	Ser	Val	
265					270					275					280	
TCA	TAT	GAT	GAA	TGG	GAC	TAT	GGC	CTC	CCC	CCC	AGA	GTG	AGA	GAT	GGA	1097
Ser	Tyr	Asp	Glu	Trp	Asp	Tyr	Gly	Leu	Pro	Pro	Arg	Val	Arg	Asp	Gly	
				285					290					295		
ATT	GCC	ATA	ATC	ACC	ACT	GCT	GCT	TCT	GAC	ATG	CTG	TCT	GAG	CAC	AGC	1145
Ile	Ala	Ile	Ile	Thr	Thr	Ala	Ala	Ser	Asp	Met	Leu	Ser	Glu	His	Ser	
			300					305					310			
TTC	ATC	CCT	GAG	CCC	AAA	AGC	AGT	TGT	TAC	AAC	ACC	CAC	GAG	AAG	AGA	1193
Phe	Ile	Pro	Glu	Pro	Lys	Ser	Ser	Cys	Tyr	Asn	Thr	His	Glu	Lys	Arg	
		315					320					325				
ATC	TAC	CAG	TCC	AAT	ATG	CTA	AAT	AGG	TAT	CTG	ATC	AAT	GTC	ACT	TTT	1241
Ile	Tyr	Gln	Ser	Asn	Met	Leu	Asn	Arg	Tyr	Leu	Ile	Asn	Val	Thr	Phe	
	330					335					340					
GAG	GGG	AGG	AAT	TTG	TCC	TTC	AGT	GAA	GAT	GGC	TAC	CAG	ATG	CAC	CCG	1289
Glu	Gly	Arg	Asn	Leu	Ser	Phe	Ser	Glu	Asp	Gly	Tyr	Gln	Met	His	Pro	
345					350					355					360	
AAA	CTG	GTG	ATA	ATT	CTT	CTG	AAC	AAG	GAG	AGG	AAG	TGG	GAA	AGG	GTG	1337
Lys	Leu	Val	Ile	Ile	Leu	Leu	Asn	Lys	Glu	Arg	Lys	Trp	Glu	Arg	Val	
				365					370					375		
GGG	AAG	TGG	AAA	GAC	AAG	TCC	CTG	CAG	ATG	AAG	TAC	TAT	GTG	TGG	CCC	1385
Gly	Lys	Trp	Lys	Asp	Lys	Ser	Leu	Gln	Met	Lys	Tyr	Tyr	Val	Trp	Pro	
			380					385					390			
CGA	ATG	TGT	CCA	GAG	ACT	GAA	GAG	CAG	GAG	GAT	GAC	CAT	CTG	AGC	ATT	1433
Arg	Met	Cys	Pro	Glu	Thr	Glu	Glu	Gln	Glu	Asp	Asp	His	Leu	Ser	Ile	
		395					400					405				

T000747-120T

GTG	ACC	CTG	GAG	GAG	GCA	CCA	TTT	GTC	ATT	GTG	GAA	AGT	GTG	GAC	CCT	1481
Val	Thr	Leu	Glu	Glu	Ala	Pro	Phe	Val	Ile	Val	Glu	Ser	Val	Asp	Pro	
	410					415					420					
CTG	AGT	GGA	ACC	TGC	ATG	AGG	AAC	ACA	GTC	CCC	TGC	CAA	AAA	CGC	ATA	1529
Leu	Ser	Gly	Thr	Cys	Met	Arg	Asn	Thr	Val	Pro	Cys	Gln	Lys	Arg	Ile	
425					430					435					440	
GTC	ACT	GAG	AAT	AAA	ACA	GAC	GAG	GAG	CCG	GGT	TAC	ATC	AAA	AAA	TGC	1577
Val	Thr	Glu	Asn	Lys	Thr	Asp	Glu	Glu	Pro	Gly	Tyr	Ile	Lys	Lys	Cys	
				445					450						455	
TGC	AAG	GGG	TTC	TGT	ATT	GAC	ATC	CTT	AAG	AAA	ATT	TCT	AAA	TCT	GTG	1625
Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Lys	Ile	Ser	Lys	Ser	Val	
			460					465						470		
AAG	TTC	ACC	TAT	GAC	CTT	TAC	CTG	GTT	ACC	AAT	GGC	AAG	CAT	GGG	AAG	1673
Lys	Phe	Thr	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn	Gly	Lys	His	Gly	Lys	
		475					480						485			
AAA	ATC	AAT	GGA	ACC	TGG	AAT	GGT	ATG	ATT	GGA	GAG	GTG	GTC	ATG	AAG	1721
Lys	Ile	Asn	Gly	Thr	Trp	Asn	Gly	Met	Ile	Gly	Glu	Val	Val	Met	Lys	
	490					495					500					
AGG	GCC	TAC	ATG	GCA	GTG	GGC	TCA	CTC	ACC	ATC	AAT	GAG	GAA	CGA	TCG	1769
Arg	Ala	Tyr	Met	Ala	Val	Gly	Ser	Leu	Thr	Ile	Asn	Glu	Glu	Arg	Ser	
505					510					515					520	
GAG	GTG	GTC	GAC	TTC	TCT	GTG	CCC	TTC	ATA	GAG	ACA	GGC	ATC	AGT	GTC	1817
Glu	Val	Val	Asp	Phe	Ser	Val	Pro	Phe	Ile	Glu	Thr	Gly	Ile	Ser	Val	
				525					530						535	
ATG	GTG	TCA	CGC	AGC	AAT	GGG	ACT	GTC	TCA	CCT	TCT	GCC	TTC	TTA	GAG	1865
Met	Val	Ser	Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro	Ser	Ala	Phe	Leu	Glu	
			540					545						550		
CCA	TTC	AGC	GCT	GAC	GTA	TGG	GTG	ATG	ATG	TTT	GTG	ATG	CTG	CTC	ATC	1913
Pro	Phe	Ser	Ala	Asp	Val	Trp	Val	Met	Met	Phe	Val	Met	Leu	Leu	Ile	
		555					560					565				
GTC	TCA	GCC	GTG	GCT	GTC	TTT	GTC	TTT	GAG	TAC	TTC	AGC	CCT	GTG	GGT	1961
Val	Ser	Ala	Val	Ala	Val	Phe	Val	Phe	Glu	Tyr	Phe	Ser	Pro	Val	Gly	
	570					575					580					
TAT	AAC	AGG	TGC	CTC	GCT	GAT	GGC	AGA	GAG	CCT	GGT	GGA	CCC	TCT	TTC	2009
Tyr	Asn	Arg	Cys	Leu	Ala	Asp	Gly	Arg	Glu	Pro	Gly	Gly	Pro	Ser	Phe	
585					590					595					600	
ACC	ATC	GGC	AAA	GCT	ATT	TGG	TTG	CTC	TGG	GGT	CTG	GTG	TTT	AAC	AAC	2057
Thr	Ile	Gly	Lys		Ile	Trp	Leu	Leu	Trp	Gly	Leu	Val	Phe	Asn	Asn	
				605					610						615	
TCC	GTA	CCT	GTG	CAG	AAC	CCA	AAG	GGG	ACC	ACC	TCC	AAG	ATC	ATG	GTG	2105
Ser	Val	Pro	Val	Gln	Asn	Pro	Lys	Gly	Thr	Thr	Ser	Lys	Ile	Met	Val	
			620					625						630		
TCA	GTG	TGG	GCC	TTC	TTT	GCT	GTC	ATC	TTC	CTG	GCC	AGC	TAC	ACT	GCC	2153
Ser	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	Ser	Tyr	Thr	Ala	
		635					640					645				
AAC	TTA	GCT	GCC	TTC	ATG	ATC	CAA	GAG	GAA	TAT	GTG	GAC	CAG	GTT	TCT	2201
Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Glu	Tyr	Val	Asp	Gln	Val	Ser	
	650					655					660					
GGC	CTG	AGC	GAC	AAA	AAG	TTC	CAG	AGA	CCT	AAT	GAC	TTC	TCA	CCC	CCT	2249
Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	Pro	Asn	Asp	Phe	Ser	Pro	Pro	
665					670					675					680	

TTC Phe	CGC Arg	TTT Phe	GGG Gly	ACC Thr 685	GTG Val	CCC Pro	AAC Asn	GGC Gly	AGC Ser 690	ACA Thr	GAG Glu	AGA Arg	AAT Asn	ATT Ile 695	CGC Arg	2297
AAT Asn	AAC Asn	TAT Tyr	GCA Ala 700	GAA Glu	ATG Met	CAT His	GCC Ala	TAC Tyr 705	ATG Met	GGA Gly	AAG Lys	TTC Phe 710	AAC Asn	CAG Gln	AGG Arg	2345
GGT Gly	GTA Val	GAT Asp 715	GAT Asp	GCA Ala	TTG Leu	CTC Leu	TCC Ser 720	CTG Leu	AAA Lys	ACA Thr	GGG Gly 725	AAA Lys	CTG Leu	GAT Asp	GCC Ala	2393
TTC Phe	ATC Ile 730	TAT Tyr	GAT Asp	GCA Ala	GCA Ala	GTG Val 735	CTG Leu	AAC Asn	TAT Tyr	ATG Met	GCA Ala 740	GGC Gly	AGA Arg	GAT Asp	GAA Glu	2441
GGC Gly 745	TGC Cys	AAG Lys	CTG Leu	GTG Val	ACC Thr 750	ATT Ile	GGC Gly	AGT Ser	GGG Gly 755	AAG Lys	GTC Val	TTT Phe	GCT Ala	TCC Ser	ACT Thr 760	2489
GGC Gly	TAT Tyr	GGC Gly	ATT Ile	GCC Ala 765	ATC Ile	CAA Gln	AAA Lys	GAT Asp 770	TCT Ser	GGG Gly	TGG Trp	AAG Lys	CGC Arg	CAG Gln 775	GTG Val	2537
GAC Asp	CTT Leu	GCT Ala	ATC Ile 780	CTG Leu	CAG Gln	CTC Leu	TTT Phe	GGA Gly 785	GAT Asp	GGG Gly	GAG Glu	ATG Met 790	GAA Glu	GAA Glu	CTG Leu	2585
GAA Glu	GCT Ala	CTC Leu 795	TGG Trp	CTC Leu	ACT Thr	GGC Gly	ATT Ile 800	TGT Cys	CAC His	AAT Asn	GAG Glu	AAG Lys 805	AAT Asn	GAG Glu	GTC Val	2633
ATG Met	AGC Ser 810	AGC Ser	CAG Gln	CTG Leu	GAC Asp	ATT Ile 815	GAC Asp	AAC Asn	ATG Met	GCA Ala 820	GGG Gly	GTC Val	TTC Phe	TAC Tyr	ATG Met	2681
TTG Leu 825	GGG Gly	GCG Ala	GCC Ala	ATG Met 830	GCT Ala	CTC Leu	AGC Ser	CTC Leu	ATC Ile	ACC Thr 835	TTC Phe	ATC Ile	TGC Cys	GAA Glu	CAC His 840	2729
CTT Leu	TTC Phe	TAT Tyr	TGG Trp 845	CAG Gln	TTC Phe	CGA Arg	CAT His	TGC Cys	TTT Phe 850	ATG Met	GGT Gly	GTC Val	TGT Cys	TCT Ser 855	GGC Gly	2777
AAG Lys	CCT Pro	GGC Gly	ATG Met 860	GTC Val	TTC Phe	TCC Ser	ATC Ile	AGC Ser 865	AGA Arg	GGT Gly	ATC Ile	TAC Tyr	AGC Ser 870	TGC Cys	ATC Ile	2825
CAT His	GGG Gly	GTG Val 875	GCG Ala	ATC Ile	GAG Glu	GAG Glu	CGC Arg 880	CAG Gln	TCT Ser	GTA Val	ATG Met 885	AAC Asn	TCC Ser	CCC Pro	ACC Thr	2873
GCA Ala	ACC Thr 890	ATG Met	AAC Asn	AAC Asn	ACA Thr	CAC His 895	TCC Ser	AAC Asn	ATC Ile	CTG Leu 900	CGC Arg	CTG Leu	CTG Leu	CGC Arg	ACG Thr	2921
GCC Ala 905	AAG Lys	AAC Asn	ATG Met	GCT Ala	AAC Asn 910	CTG Leu	TCT Ser	GGT Gly	GTG Val 915	AAT Asn	GGC Gly	TCA Ser	CCG Pro	CAG Gln	AGC Ser 920	2969
GCC Ala	CTG Leu	GAC Asp	TTC Phe 925	ATC Ile	CGA Arg	CGG Arg	GAG Glu	TCA Ser 930	TCC Ser	GTC Val	TAT Tyr	GAC Asp	ATC Ile	TCA Ser 935	GAG Glu	3017
CAC His	CGC Arg	CGC Arg	AGC Ser 940	TTC Phe	ACG Thr	CAT His	TCT Ser	GAC Asp 945	TGC Cys	AAA Lys	TCC Ser	TAC Tyr	AAC Asn 950	AAC Asn	CCG Pro	3065

CCC TGT GAG GAG AAC CTC TTC AGT GAC TAC ATC AGT GAG GTA GAG AGA Pro Cys Glu Glu Asn Leu Phe Ser Asp Tyr Ile Ser Glu Val Glu Arg 955 960 965	3113
ACG TTC GGG AAC CTG CAG CTG AAG GAC AGC AAC GTG TAC CAA GAT CAC Thr Phe Gly Asn Leu Gln Leu Lys Asp Ser Asn Val Tyr Gln Asp His 970 975 980	3161
TAC CAC CAT CAC CAC CGG CCC CAT AGT ATT GGC AGT GCC AGC TCC ATC Tyr His His His His Arg Pro His Ser Ile Gly Ser Ala Ser Ser Ile 985 990 995 1000	3209
GAT GGG CTC TAC GAC TGT GAC AAC CCA CCC TTC ACC ACC CAG TCC AGG Asp Gly Leu Tyr Asp Cys Asp Asn Pro Pro Phe Thr Thr Gln Ser Arg 1005 1010 1015	3257
TCC ATC AGC AAG AAG CCC CTG GAC ATC GGC CTC CCC TCC TCC AAG CAC Ser Ile Ser Lys Lys Pro Leu Asp Ile Gly Leu Pro Ser Ser Lys His 1020 1025 1030	3305
AGC CAG CTC AGT GAC CTG TAC GGC AAA TTC TCC TTC AAG AGC GAC CGC Ser Gln Leu Ser Asp Leu Tyr Gly Lys Phe Ser Phe Lys Ser Asp Arg 1035 1040 1045	3353
TAC AGT GGC CAC GAC GAC TTG ATC CGC TCC GAT GTC TCT GAC ATC TCA Tyr Ser Gly His Asp Asp Leu Ile Arg Ser Asp Val Ser Asp Ile Ser 1050 1055 1060	3401
ACC CAC ACC GTC ACC TAT GGG AAC ATC GAG GGC AAT GCC GCC AAG AGG Thr His Thr Val Thr Tyr Gly Asn Ile Glu Gly Asn Ala Ala Lys Arg 1065 1070 1075 1080	3449
CGT AAG CAG CAA TAT AAG GAC AGC CTG AAG AAG CGG CCT GCC TCG GCC Arg Lys Gln Gln Tyr Lys Asp Ser Leu Lys Lys Arg Pro Ala Ser Ala 1085 1090 1095	3497
AAG TCC CGC AGG GAG TTT GAC GAG ATC GAG CTG GCC TAC CGT CGC CGA Lys Ser Arg Arg Glu Phe Asp Glu Ile Glu Leu Ala Tyr Arg Arg Arg 1100 1105 1110	3545
CCG CCC CGC TCC CCT GAC CAC AAG CGC TAC TTC AGG GAC AAG GAA GGG Pro Pro Arg Ser Pro Asp His Lys Arg Tyr Phe Arg Asp Lys Glu Gly 1115 1120 1125	3593
CTA CGG GAC TTC TAC CTG GAC CAG TTC CGA ACA AAG GAG AAC TCA CCC Leu Arg Asp Phe Tyr Leu Asp Gln Phe Arg Thr Lys Glu Asn Ser Pro 1130 1135 1140	3641
CAC TGG GAG CAC GTA GAC CTG ACC GAC ATC TAC AAG GAG CGG AGT GAT His Trp Glu His Val Asp Leu Thr Asp Ile Tyr Lys Glu Arg Ser Asp 1145 1150 1155 1160	3689
GAC TTT AAG CGC GAC TCC ATC AGC GGA GGA GGG CCC TGT ACC AAC AGG Asp Phe Lys Arg Asp Ser Ile Ser Gly Gly Gly Pro Cys Thr Asn Arg 1165 1170 1175	3737
TCT CAC ATC AAG CAC GGG ACG GGC GAC AAA CAC GGC GTG GTC AGC GGG Ser His Ile Lys His Gly Thr Gly Asp Lys His Gly Val Val Ser Gly 1180 1185 1190	3785
GTA CCT GCA CCT TGG GAG AAG AAC CTG ACC AAC GTG GAG TGG GAG GAC Val Pro Ala Pro Trp Glu Lys Asn Leu Thr Asn Val Glu Trp Glu Asp 1195 1200 1205	3833
CGG TCC GGG GGC AAC TTC TGC CGC AGC TGT CCC TCC AAG CTG CAC AAC Arg Ser Gly Gly Asn Phe Cys Arg Ser Cys Pro Ser Lys Leu His Asn 1210 1215 1220	3881

1000747-12001

TAC TCC ACG ACG GTG ACG GGT CAG AAC TCG GGC AGG CAG GCG TGC ATC Tyr Ser Thr Thr Val Thr Gly Gln Asn Ser Gly Arg Gln Ala Cys Ile 1225 1230 1235 1240	3929
CGG TGT GAG GCT TGC AAG AAA GCA GGC AAC CTG TAT GAC ATC AGT GAG Arg Cys Glu Ala Cys Lys Lys Ala Gly Asn Leu Tyr Asp Ile Ser Glu 1245 1250 1255	3977
GAC AAC TCC CTG CAG GAA CTG GAC CAG CCG GCT GCC CCA GTG GCG GTG Asp Asn Ser Leu Gln Glu Leu Asp Gln Pro Ala Ala Pro Val Ala Val 1260 1265 1270	4025
ACG TCA AAC GCC TCC ACC ACT AAG TAC CCT CAG AGC CCG ACT AAT TCC Thr Ser Asn Ala Ser Thr Thr Lys Tyr Pro Gln Ser Pro Thr Asn Ser 1275 1280 1285	4073
AAG GCC CAG AAG AAG AAC CGG AAC AAA CTG CGC CGG CAG CAC TCC TAC Lys Ala Gln Lys Lys Asn Arg Asn Lys Leu Arg Arg Gln His Ser Tyr 1290 1295 1300	4121
GAC ACC TTC GTG GAC CTG CAG AAG GAA GAA GCC GCC CTG GCC CCG CGC Asp Thr Phe Val Asp Leu Gln Lys Glu Glu Ala Ala Leu Ala Pro Arg 1305 1310 1315 1320	4169
AGC GTA AGC CTG AAA GAC AAG GGC CGA TTC ATG GAT GGG AGC CCC TAC Ser Val Ser Leu Lys Asp Lys Gly Arg Phe Met Asp Gly Ser Pro Tyr 1325 1330 1335	4217
GCC CAC ATG TTT GAG ATG TCA GCT GGC GAG AGC ACC TTT GCC AAC AAC Ala His Met Phe Glu Met Ser Ala Gly Glu Ser Thr Phe Ala Asn Asn 1340 1345 1350	4265
AAG TCC TCA GTG CCC ACT GCC GGA CAT CAC CAC CAC AAC AAC CCC GGC Lys Ser Ser Val Pro Thr Ala Gly His His His His Asn Asn Pro Gly 1355 1360 1365	4313
GGC GGG TAC ATG CTC AGC AAG TCG CTC TAC CCT GAC CGG GTC ACG CAA Gly Gly Tyr Met Leu Ser Lys Ser Leu Tyr Pro Asp Arg Val Thr Gln 1370 1375 1380	4361
AAC CCT TTC ATC CCC ACT TTT GGG GAC GAC CAG TGC TTG CTC CAT GGC Asn Pro Phe Ile Pro Thr Phe Gly Asp Asp Gln Cys Leu Leu His Gly 1385 1390 1395 1400	4409
AGC AAA TCC TAC TTC TTC AGG CAG CCC ACG GTG GCG GGG GCG TCG AAA Ser Lys Ser Tyr Phe Phe Arg Gln Pro Thr Val Ala Gly Ala Ser Lys 1405 1410 1415	4457
GCC AGG CCG GAC TTC CGG GCC CTT GTC ACC AAC AAG CCG GTG GTC TCG Ala Arg Pro Asp Phe Arg Ala Leu Val Thr Asn Lys Pro Val Val Ser 1420 1425 1430	4505
GCC CTT CAT GGG GCC GTG CCA GCC CGT TTC CAG AAG GAC ATC TGT ATA Ala Leu His Gly Ala Val Pro Ala Arg Phe Gln Lys Asp Ile Cys Ile 1435 1440 1445	4553
GGG AAC CAG TCC AAC CCC TGT GTG CCT AAC AAC ACA AAC CCC AGG GCT Gly Asn Gln Ser Asn Pro Cys Val Pro Asn Asn Thr Asn Pro Arg Ala 1450 1455 1460	4601
TTC AAT GGC TCC AGC AAT GGG CAT GTT TAT GAG AAA CTT TCT AGT ATT Phe Asn Gly Ser Ser Asn Gly His Val Tyr Glu Lys Leu Ser Ser Ile 1465 1470 1475 1480	4649
GAG TCT GAT GTC TGAGTGAGGG AACAGAGAGG TTAAGGTGGG TACGGGAGGG Glu Ser Asp Val	4701

TAAGGCTGTG GGTCGCGTGA TGCGCATGTC ACGGAGGGTG ACGGGGGTGA ACTTG GTTCC 4761
 CATTTGCTCC TTTCTTGTTT TAATTTATTT ATGGGATCCT GGAGTTCTGG TTCCTACTGG 4821
 GGGCAACCCT GGTGACCAGC ACCATCTCTC CTCCTTTTCA CAGTTCTCTC CTTCTTCCCC 4881
 CCGCTGTCAG CCATTCCTGT TCCCATGAGA TGATGCCATG GGCCCTCTCA GCAGGGGAGG 4941
 GTAGAGCGGA GAAAGGAAGG GCTGCATGCG GGCTTCCTCC TGGTGTGGAA GAGCTCCTTG 5001
 ATATCCTCTT TGAGTGAAGC TGGGAGAACC AAAAAGAGGC TATGTGAGCA CAAAGGTAGC 5061
 TTTTCCCAA CTGATCTTTT CATTTAGGTG AGGAAGCAAA AGCATCTATG TGAGACCATT 5121
 TAGCACACTG CTTGTGAAAG GAAAGAGGCT CTGGCTAAAT TCATGCTGCT TAGATGACAT 5181
 CTGTCTAGGA ATCATGTGCC AAGCAGAGGT TGGGAGGCCA TTTGTGTTTA TATATAAGCC 5241
 CAAAATGCT TGCTTCAACC CCATGAGACT CGATAGTGGT GGTGAACAGA ACCCAAGGTC 5301
 ATTGGTGGCA GAGTGGATTC TTGAACAAAC TGGAAAGTAC GTTATGATAG TGTCCCCCGG 5361
 TGCCTTGGGG ACAAGAGCAG GTGGATTGTG CGTGCATGTG TGTTTCATGCA CACTTGCACC 5421
 CATGTGTAGT CAGGTGCCTC AAGAGAAGGC AACCTTGACT CTTTCGTTGA ATTTGCATCT 5481
 CTTCAAGACA CAAGATTAAA ACAAATTTA CGCTAAATTG GATTTTAAAT TATCTTC 5538

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Lys Pro Arg Ala Glu Cys Cys Ser Pro Lys Phe Trp Leu Val Leu
 1 5 10 15
 Ala Val Leu Ala Val Ser Gly Ser Arg Ala Arg Ser Gln Lys Ser Pro
 20 25 30
 Pro Ser Ile Gly Ile Ala Val Ile Leu Val Gly Thr Ser Asp Glu Val
 35 40 45
 Ala Ile Lys Asp Ala His Glu Lys Asp Asp Phe His His Leu Ser Val
 50 55 60
 Val Pro Arg Val Glu Leu Val Ala Met Asn Glu Thr Asp Pro Lys Ser
 65 70 75 80
 Ile Ile Thr Arg Ile Cys Asp Leu Met Ser Asp Arg Lys Ile Gln Gly
 85 90 95
 Val Val Phe Ala Asp Asp Thr Asp Gln Glu Ala Ile Ala Gln Ile Leu
 100 105 110
 Asp Phe Ile Ser Ala Gln Thr Leu Thr Pro Ile Leu Gly Ile His Gly
 115 120 125
 Gly Ser Ser Met Ile Met Ala Asp Lys Asp Glu Ser Ser Met Phe Phe
 130 135 140

1000747-12001

Gln Phe Gly Pro Ser Ile Glu Gln Gln Ala Ser Val Met Leu Asn Ile
 145 150 155 160
 Met Glu Glu Tyr Asp Trp Tyr Ile Phe Ser Ile Val Thr Thr Tyr Phe
 165 170 175
 Pro Gly Tyr Gln Asp Phe Val Asn Lys Ile Arg Ser Thr Ile Glu Asn
 180 185 190
 Ser Phe Val Gly Trp Glu Leu Glu Glu Val Leu Leu Leu Asp Met Ser
 195 200 205
 Leu Asp Asp Gly Asp Ser Lys Ile Gln Asn Gln Leu Lys Lys Leu Gln
 210 215 220
 Ser Pro Ile Ile Leu Leu Tyr Cys Thr Lys Glu Glu Ala Thr Tyr Ile
 225 230 235 240
 Phe Glu Val Ala Asn Ser Val Gly Leu Thr Gly Tyr Gly Tyr Thr Trp
 245 250 255
 Ile Val Pro Ser Leu Val Ala Gly Asp Thr Asp Thr Val Pro Ala Glu
 260 265 270
 Phe Pro Thr Gly Leu Ile Ser Val Ser Tyr Asp Glu Trp Asp Tyr Gly
 275 280 285
 Leu Pro Pro Arg Val Arg Asp Gly Ile Ala Ile Ile Thr Thr Ala Ala
 290 295 300
 Ser Asp Met Leu Ser Glu His Ser Phe Ile Pro Glu Pro Lys Ser Ser
 305 310 315 320
 Cys Tyr Asn Thr His Glu Lys Arg Ile Tyr Gln Ser Asn Met Leu Asn
 325 330 335
 Arg Tyr Leu Ile Asn Val Thr Phe Glu Gly Arg Asn Leu Ser Phe Ser
 340 345 350
 Glu Asp Gly Tyr Gln Met His Pro Lys Leu Val Ile Ile Leu Leu Asn
 355 360 365
 Lys Glu Arg Lys Trp Glu Arg Val Gly Lys Trp Lys Asp Lys Ser Leu
 370 375 380
 Gln Met Lys Tyr Tyr Val Trp Pro Arg Met Cys Pro Glu Thr Glu Glu
 385 390 395 400
 Gln Glu Asp Asp His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe
 405 410 415
 Val Ile Val Glu Ser Val Asp Pro Leu Ser Gly Thr Cys Met Arg Asn
 420 425 430
 Thr Val Pro Cys Gln Lys Arg Ile Val Thr Glu Asn Lys Thr Asp Glu
 435 440 445
 Glu Pro Gly Tyr Ile Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile
 450 455 460
 Leu Lys Lys Ile Ser Lys Ser Val Lys Phe Thr Tyr Asp Leu Tyr Leu
 465 470 475 480
 Val Thr Asn Gly Lys His Gly Lys Lys Ile Asn Gly Thr Trp Asn Gly
 485 490 495

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 10007424001

Met Ile Gly Glu Val Val Met Lys Arg Ala Tyr Met Ala Val Gly Ser
500 505 510

Leu Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro
515 520 525

Phe Ile Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr
530 535 540

Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Asp Val Trp Val
545 550 555 560

Met Met Phe Val Met Leu Leu Ile Val Ser Ala Val Ala Val Phe Val
565 570 575

Phe Glu Tyr Phe Ser Pro Val Gly Tyr Asn Arg Cys Leu Ala Asp Gly
580 585 590

Arg Glu Pro Gly Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu
595 600 605

Leu Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys
610 615 620

Gly Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val
625 630 635 640

Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln
645 650 655

Glu Glu Tyr Val Asp Gln Val Ser Gly Leu Ser Asp Lys Lys Phe Gln
660 665 670

Arg Pro Asn Asp Phe Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn
675 680 685

Gly Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Ala Glu Met His Ala
690 695 700

Tyr Met Gly Lys Phe Asn Gln Arg Gly Val Asp Asp Ala Leu Leu Ser
705 710 715 720

Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu
725 730 735

Asn Tyr Met Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly
740 745 750

Ser Gly Lys Val Phe Ala Ser Thr Gly Tyr Gly Ile Ala Ile Gln Lys
755 760 765

Asp Ser Gly Trp Lys Arg Gln Val Asp Leu Ala Ile Leu Gln Leu Phe
770 775 780

Gly Asp Gly Glu Met Glu Glu Leu Glu Ala Leu Trp Leu Thr Gly Ile
785 790 795 800

Cys His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp
805 810 815

Asn Met Ala Gly Val Phe Tyr Met Leu Gly Ala Ala Met Ala Leu Ser
820 825 830

Leu Ile Thr Phe Ile Cys Glu His Leu Phe Tyr Trp Gln Phe Arg His
835 840 845

1000747-120701

Cys	Phe	Met	Gly	Val	Cys	Ser	Gly	Lys	Pro	Gly	Met	Val	Phe	Ser	Ile	850	855	860
Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Ile	His	Gly	Val	Ala	Ile	Glu	Glu	Arg	865	870	875
Gln	Ser	Val	Met	Asn	Ser	Pro	Thr	Ala	Thr	Met	Asn	Asn	Thr	His	Ser	885	890	895
Asn	Ile	Leu	Arg	Leu	Leu	Arg	Thr	Ala	Lys	Asn	Met	Ala	Asn	Leu	Ser	900	905	910
Gly	Val	Asn	Gly	Ser	Pro	Gln	Ser	Ala	Leu	Asp	Phe	Ile	Arg	Arg	Glu	915	920	925
Ser	Ser	Val	Tyr	Asp	Ile	Ser	Glu	His	Arg	Arg	Ser	Phe	Thr	His	Ser	930	935	940
Asp	Cys	Lys	Ser	Tyr	Asn	Asn	Pro	Pro	Cys	Glu	Glu	Asn	Leu	Phe	Ser	945	950	955
Asp	Tyr	Ile	Ser	Glu	Val	Glu	Arg	Thr	Phe	Gly	Asn	Leu	Gln	Leu	Lys	965	970	975
Asp	Ser	Asn	Val	Tyr	Gln	Asp	His	Tyr	His	His	His	His	Arg	Pro	His	980	985	990
Ser	Ile	Gly	Ser	Ala	Ser	Ser	Ile	Asp	Gly	Leu	Tyr	Asp	Cys	Asp	Asn	995	1000	1005
Pro	Pro	Phe	Thr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Lys	Lys	Pro	Leu	Asp	1010	1015	1020
Ile	Gly	Leu	Pro	Ser	Ser	Lys	His	Ser	Gln	Leu	Ser	Asp	Leu	Tyr	Gly	1025	1030	1035
Lys	Phe	Ser	Phe	Lys	Ser	Asp	Arg	Tyr	Ser	Gly	His	Asp	Asp	Leu	Ile	1045	1050	1055
Arg	Ser	Asp	Val	Ser	Asp	Ile	Ser	Thr	His	Thr	Val	Thr	Tyr	Gly	Asn	1060	1065	1070
Ile	Glu	Gly	Asn	Ala	Ala	Lys	Arg	Arg	Lys	Gln	Gln	Tyr	Lys	Asp	Ser	1075	1080	1085
Leu	Lys	Lys	Arg	Pro	Ala	Ser	Ala	Lys	Ser	Arg	Arg	Glu	Phe	Asp	Glu	1090	1095	1100
Ile	Glu	Leu	Ala	Tyr	Arg	Arg	Arg	Pro	Pro	Arg	Ser	Pro	Asp	His	Lys	1105	1110	1115
Arg	Tyr	Phe	Arg	Asp	Lys	Glu	Gly	Leu	Arg	Asp	Phe	Tyr	Leu	Asp	Gln	1125	1130	1135
Phe	Arg	Thr	Lys	Glu	Asn	Ser	Pro	His	Trp	Glu	His	Val	Asp	Leu	Thr	1140	1145	1150
Asp	Ile	Tyr	Lys	Glu	Arg	Ser	Asp	Asp	Phe	Lys	Arg	Asp	Ser	Ile	Ser	1155	1160	1165
Gly	Gly	Gly	Pro	Cys	Thr	Asn	Arg	Ser	His	Ile	Lys	His	Gly	Thr	Gly	1170	1175	1180
Asp	Lys	His	Gly	Val	Val	Ser	Gly	Val	Pro	Ala	Pro	Trp	Glu	Lys	Asn	1185	1190	1195

Leu Thr Asn Val Glu Trp Glu Asp Arg Ser Gly Gly Asn Phe Cys Arg
 1205 1210 1215
 Ser Cys Pro Ser Lys Leu His Asn Tyr Ser Thr Thr Val Thr Gly Gln
 1220 1225 1230
 Asn Ser Gly Arg Gln Ala Cys Ile Arg Cys Glu Ala Cys Lys Lys Ala
 1235 1240 1245
 Gly Asn Leu Tyr Asp Ile Ser Glu Asp Asn Ser Leu Gln Glu Leu Asp
 1250 1255 1260
 Gln Pro Ala Ala Pro Val Ala Val Thr Ser Asn Ala Ser Thr Thr Lys
 1265 1270 1275 1280
 Tyr Pro Gln Ser Pro Thr Asn Ser Lys Ala Gln Lys Lys Asn Arg Asn
 1285 1290 1295
 Lys Leu Arg Arg Gln His Ser Tyr Asp Thr Phe Val Asp Leu Gln Lys
 1300 1305 1310
 Glu Glu Ala Ala Leu Ala Pro Arg Ser Val Ser Leu Lys Asp Lys Gly
 1315 1320 1325
 Arg Phe Met Asp Gly Ser Pro Tyr Ala His Met Phe Glu Met Ser Ala
 1330 1335 1340
 Gly Glu Ser Thr Phe Ala Asn Asn Lys Ser Ser Val Pro Thr Ala Gly
 1345 1350 1355 1360
 His His His His Asn Asn Pro Gly Gly Gly Tyr Met Leu Ser Lys Ser
 1365 1370 1375
 Leu Tyr Pro Asp Arg Val Thr Gln Asn Pro Phe Ile Pro Thr Phe Gly
 1380 1385 1390
 Asp Asp Gln Cys Leu Leu His Gly Ser Lys Ser Tyr Phe Phe Arg Gln
 1395 1400 1405
 Pro Thr Val Ala Gly Ala Ser Lys Ala Arg Pro Asp Phe Arg Ala Leu
 1410 1415 1420
 Val Thr Asn Lys Pro Val Val Ser Ala Leu His Gly Ala Val Pro Ala
 1425 1430 1435 1440
 Arg Phe Gln Lys Asp Ile Cys Ile Gly Asn Gln Ser Asn Pro Cys Val
 1445 1450 1455
 Pro Asn Asn Thr Asn Pro Arg Ala Phe Asn Gly Ser Ser Asn Gly His
 1460 1465 1470
 Val Tyr Glu Lys Leu Ser Ser Ile Glu Ser Asp Val
 1475 1480

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

1000747-12001

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 485..4495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGAGAACACA GCGAGTGTGT GAGTCCCTCC CGCTCCAGCT CCTCCAAGCC GCGGCCGCCG	60
CCGCCACCCT CGCCCGCAGC CTCCCGCAGC CTCCCTCGGC CACCGGTGTC TGGTGGGGGT	120
GTTGCCTGGG TAGGTCGGCC CGGCCCCAG GGGTCTCTCG AGCGTCTGCC ATCTGCCCCA	180
GAAACATGTG TGGCCACGTC CTCGCCTAGT CCAGGTGGCC GCAACCTTGG GGGAGAGACA	240
GGGCAGGACA GGACCAAGGT AAGAGGTAAG GAGGAGACGG CGCCAGGGAC AGACAGGAGG	300
TCCCGGCTTG CCGTTGTGCG CACCACCACT GCCGCCGCC CGGGGCCTGC CCCCACATC	360
GGCTCTCTGA GCCCTCCTCG GAATCTTGGG GTCGCTGGAC GCCGGGTTC GGTCTTGCC	420
CCCCCGCCAT CCCCCAACA GAACAGGGTC ATGAAAGAG GCCGCCCGGC GGGGCCCGCA	480
GGCG ATG CGC GGC GCC GGT GGC CCC CGC GGC CCT CGG GGC CCC GCT AAG	529
Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys	
1 5 10 15	
ATG CTG CTG CTG CTG GCG CTG GCC TGC GCC AGC CCG TTC CCG GAG GAG	577
Met Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu	
20 25 30	
GCG CCG GGG CCG GGC GGG GCC GGT GGG CCC GGC GGC GGC CTC GGC GGG	625
Ala Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly	
35 40 45	
GCG CCG CCG CTC AAC GTG GCG CTC GTG TTC TCG GGG CCC GCG TAC GCG	673
Ala Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala	
50 55 60	
GCC GAG GCG GCA CGC CTG GGC CCG GCC GTG GCG GCG GCG GTG CGC AGC	721
Ala Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Ala Val Arg Ser	
65 70 75	
CCG GGC CTA GAC GTG CGG CCC GTG GCG CTG GTG CTC AAC GGC TCG GAC	769
Pro Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp	
80 85 90 95	
CCG CGC AGC CTC GTG CTG CAG CTC TGC GAC CTG CTG TCG GGG TTG CGC	817
Pro Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg	
100 105 110	
GTG CAC GGC GTG GTC TTC GAA GAC GAC TCG CGC GCG CCC GCC GTC GCG	865
Val His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala	
115 120 125	
CCC ATC CTC GAC TTC CTG TCG GCG CAG ACC TCG CTC CCC ATC GTG TCC	913
Pro Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser	
130 135 140	
GAG CAC GGC GGC GCC GCG CTC GTG CTC ACG CCC AAG GAG AAG GGC TCC	961
Glu His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser	
145 150 155	
ACC TTC CTC CAC CTG GGC TCT TCC CCC GAG CAA CAG CTT CAG GTC ATC	1009
Thr Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile	
160 165 170 175	

10007747-120701

TTT	GAG	GTG	CTG	GAG	GAG	TAT	GAC	TGG	ACG	TCC	TTT	GTA	GCC	GTG	ACC	1057
Phe	Glu	Val	Leu	Glu	Glu	Tyr	Asp	Trp	Thr	Ser	Phe	Val	Ala	Val	Thr	
			180						185					190		
ACT	CGT	GCC	CCT	GGC	CAC	CGG	GCC	TTC	CTG	TCC	TAC	ATT	GAG	GTG	CTG	1105
Thr	Arg	Ala	Pro	Gly	His	Arg	Ala	Phe	Leu	Ser	Tyr	Ile	Glu	Val	Leu	
			195					200					205			
ACT	GAC	GGC	AGT	CTG	GTG	GGC	TGG	GAG	CAC	CGC	GGA	GCG	CTG	ACG	CTG	1153
Thr	Asp	Gly	Ser	Leu	Val	Gly	Trp	Glu	His	Arg	Gly	Ala	Leu	Thr	Leu	
		210					215					220				
GAC	CCT	GGG	GCG	GGC	GAG	GCC	GTG	CTC	AGT	GCC	CAG	CTC	CGC	AGT	GTC	1201
Asp	Pro	Gly	Ala	Gly	Glu	Ala	Val	Leu	Ser	Ala	Gln	Leu	Arg	Ser	Val	
	225					230					235					
AGC	GCG	CAG	ATC	CGC	CTG	CTC	TTC	TGC	GCC	CGA	GAG	GAG	GCC	GAG	CCC	1249
Ser	Ala	Gln	Ile	Arg	Leu	Leu	Phe	Cys	Ala	Arg	Glu	Glu	Ala	Glu	Pro	
	240				245					250					255	
GTG	TTC	CGC	GCA	GCT	GAG	GAG	GCT	GGC	CTC	ACT	GGA	TCT	GGC	TAC	GTC	1297
Val	Phe	Arg	Ala	Ala	Glu	Glu	Ala	Gly	Leu	Thr	Gly	Ser	Gly	Tyr	Val	
			260						265					270		
TGG	TTC	ATG	GTG	GGG	CCC	CAG	CTG	GCT	GGA	GGC	GGG	GGC	TCT	GGG	GCC	1345
Trp	Phe	Met	Val	Gly	Pro	Gln	Leu	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Ala	
			275					280					285			
CCT	GGT	GAG	CCC	CCT	CTT	CTG	CCA	GGA	GGC	GCC	CCC	CTG	CCT	GCC	GGG	1393
Pro	Gly	Glu	Pro	Pro	Leu	Leu	Pro	Gly	Gly	Ala	Pro	Leu	Pro	Ala	Gly	
		290					295					300				
CTG	TTT	GCA	GTG	CGC	TCG	GCT	GGC	TGG	CGG	GAT	GAC	CTG	GCT	CGG	CGA	1441
Leu	Phe	Ala	Val	Arg	Ser	Ala	Gly	Trp	Arg	Asp	Asp	Leu	Ala	Arg	Arg	
	305					310					315					
GTG	GCA	GCT	GGC	GTG	GCC	GTA	GTG	GCC	AGA	GGT	GCC	CAG	GCC	CTG	CTG	1489
Val	Ala	Ala	Gly	Val	Ala	Val	Val	Ala	Arg	Gly	Ala	Gln	Ala	Leu	Leu	
	320				325					330				335		
CGT	GAT	TAT	GGT	TTC	CTT	CCT	GAG	CTC	GGC	CAC	GAC	TGT	CGC	GCC	CAG	1537
Arg	Asp	Tyr	Gly	Phe	Leu	Pro	Glu	Leu	Gly	His	Asp	Cys	Arg	Ala	Gln	
			340						345					350		
AAC	CGC	ACC	CAC	CGC	GGG	GAG	AGT	CTG	CAT	AGG	TAC	TTC	ATG	AAC	ATC	1585
Asn	Arg	Thr	His	Arg	Gly	Glu	Ser	Leu	His	Arg	Tyr	Phe	Met	Asn	Ile	
			355					360					365			
ACG	TGG	GAT	AAC	CGG	GAT	TAC	TCC	TTC	AAT	GAG	GAC	GGC	TTC	CTA	GTG	1633
Thr	Trp	Asp	Asn	Arg	Asp	Tyr	Ser	Phe	Asn	Glu	Asp	Gly	Phe	Leu	Val	
		370					375					380				
AAC	CCC	TCC	CTG	GTG	GTC	ATC	TCC	CTC	ACC	AGA	GAC	AGG	ACG	TGG	GAG	1681
Asn	Pro	Ser	Leu	Val	Val	Ile	Ser	Leu	Thr	Arg	Asp	Arg	Thr	Trp	Glu	
	385					390					395					
GTG	GTG	GGC	AGC	TGG	GAG	CAG	CAG	ACG	CTC	CGC	CTC	AAG	TAC	CCG	CTG	1729
Val	Val	Gly	Ser	Trp	Glu	Gln	Gln	Thr	Leu	Arg	Leu	Lys	Tyr	Pro	Leu	
	400				405					410				415		
TGG	TCC	CGC	TAT	GGT	CGC	TTC	CTG	CAG	CCA	GTG	GAC	GAC	ACG	CAG	CAC	1777
Trp	Ser	Arg	Tyr	Gly	Arg	Phe	Leu	Gln	Pro	Val	Asp	Asp	Thr	Gln	His	
			420						425					430		
CTC	GCG	GTG	GCC	ACG	CTG	GAG	GAA	AGG	CCG	TTT	GTC	ATC	GTG	GAG	CCT	1825
Leu	Ala	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	Ile	Val	Glu	Pro	
			435					440					445			

GCA	GAC	CCT	ATC	AGC	GGC	ACC	TGC	ATC	CGA	GAC	TCC	GTC	CCC	TGC	CGG	1873
Ala	Asp	Pro	Ile	Ser	Gly	Thr	Cys	Ile	Arg	Asp	Ser	Val	Pro	Cys	Arg	
		450					455					460				
AGC	CAG	CTC	AAC	CGA	ACC	CAC	AGC	CCT	CCA	CCG	GAT	GCC	CCC	CGC	CCG	1921
Ser	Gln	Leu	Asn	Arg	Thr	His	Ser	Pro	Pro	Pro	Asp	Ala	Pro	Arg	Pro	
	465					470					475					
GAA	AAG	CGC	TGC	TGC	AAG	GGT	TTC	TGC	ATC	GAC	ATT	CTG	AAG	CGG	CTG	1969
Glu	Lys	Arg	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Arg	Leu	
480					485					490					495	
GCG	CAT	ACC	ATC	GGC	TTC	AGC	TAC	GAC	CTC	TAC	CTG	GTC	ACC	AAT	GGC	2017
Ala	His	Thr	Ile	Gly	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn	Gly	
				500					505					510		
AAG	CAC	GGA	AAG	AAG	ATC	GAT	GGC	GTC	TGG	AAC	GGC	ATG	ATC	GGG	GAG	2065
Lys	His	Gly	Lys	Lys	Ile	Asp	Gly	Val	Trp	Asn	Gly	Met	Ile	Gly	Glu	
			515					520					525			
GTG	TTC	TAC	CAG	CGC	GCA	GAC	ATG	GCC	ATC	GGC	TCC	CTC	ACC	ATC	AAC	2113
Val	Phe	Tyr	Gln	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	Thr	Ile	Asn	
		530					535					540				
GAG	GAG	CGC	TCC	GAG	ATC	GTG	GAC	TTC	TCC	GTC	CCC	TTC	GTG	GAG	ACC	2161
Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	Val	Glu	Thr	
	545					550					555					
GGC	ATC	AGC	GTC	ATG	GTG	GCG	CGC	AGC	AAT	GGC	ACG	GTG	TCC	CCC	TCG	2209
Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro	Ser	
560					565					570					575	
GCC	TTC	CTC	GAG	CCC	TAC	AGC	CCC	GCC	GTG	TGG	GTG	ATG	ATG	TTC	GTC	2257
Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	Met	Phe	Val	
				580					585					590		
ATG	TGC	CTC	ACT	GTG	GTC	GCC	GTC	ACT	GTT	TTC	ATC	TTC	GAG	TAC	CTC	2305
Met	Cys	Leu	Thr	Val	Val	Ala	Val	Thr	Val	Phe	Ile	Phe	Glu	Tyr	Leu	
			595					600					605			
AGT	CCT	GTT	GGT	TAC	AAC	CGC	AGC	CTG	GCC	ACG	GGC	AAG	CGC	CCT	GGC	2353
Ser	Pro	Val	Gly	Tyr	Asn	Arg	Ser	Leu	Ala	Thr	Gly	Lys	Arg	Pro	Gly	
		610					615					620				
GGT	TCA	ACC	TTC	ACC	ATT	GGG	AAA	TCC	ATC	TGG	CTG	CTC	TGG	GCC	CTG	2401
Gly	Ser	Thr	Phe	Thr	Ile	Gly	Lys	Ser	Ile	Trp	Leu	Leu	Trp	Ala	Leu	
	625					630					635					
GTG	TTC	AAT	AAT	TCG	GTG	CCC	GTG	GAG	AAC	CCC	CGG	GGA	ACC	ACC	AGC	2449
Val	Phe	Asn	Asn	Ser	Val	Pro	Val	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser	
640					645					650					655	
AAA	ATC	ATG	GTG	CTG	GTG	TGG	GCC	TTC	TTC	GCC	GTC	ATC	TTC	CTC	GCC	2497
Lys	Ile	Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	
				660					665					670		
AGC	TAC	ACA	GCC	AAC	CTG	GCC	GCC	TTC	ATG	ATC	CAG	GAG	GAG	TAC	GTG	2545
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Glu	Tyr	Val	
			675					680					685			
GAT	ACT	GTG	TCT	GGG	CTC	AGT	GAC	CGC	AAG	TTC	CAG	AGG	CCC	CAG	GAG	2593
Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Arg	Lys	Phe	Gln	Arg	Pro	Gln	Glu	
		690					695					700				
CAG	TAC	CCG	CCC	CTG	AAG	TTT	GGG	ACC	GTG	CCC	AAC	GGC	TCC	ACG	GAG	2641
Gln	Tyr	Pro	Pro	Leu	Lys	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	
	705					710					715					

AAG Lys 720	AAC Asn	ATC Ile	CGC Arg	AGC Ser	AAC Asn 725	TAT Tyr	CCC Pro	GAC Asp	ATG Met	CAC His 730	AGC Ser	TAC Tyr	ATG Met	GTG Val	CGC Arg 735	2689
TAC Tyr	AAC Asn	CAG Gln	CCC Pro	CGC Arg 740	GTA Val	GAG Glu	GAA Glu	GCG Ala	CTC Leu 745	ACT Thr	CAG Gln	CTC Leu	AAG Lys	GCA Ala 750	GGG Gly	2737
AAG Lys	CTG Leu	GAC Asp	GCC Ala 755	TTC Phe	ATC Ile	TAC Tyr	GAT Asp	GCT Ala 760	GCA Ala	GTG Val	CTC Leu	AAT Asn 765	TAC Tyr	ATG Met	GCC Ala	2785
CGC Arg	AAG Lys	GAC Asp 770	GAG Glu	GGC Gly	TGC Cys	AAG Lys	CTT Leu 775	GTC Val	ACC Thr	ATC Ile	GGC Gly 780	TCC Ser	GGC Gly	AAG Lys	GTC Val	2833
TTC Phe 785	GCC Ala	ACG Thr	ACA Thr	GGC Gly	TAT Tyr	GGC Gly 790	ATC Ile	GCC Ala	CTG Leu	CAC His	AAG Lys 795	GGC Gly	TCC Ser	CGC Arg	TGG Trp	2881
AAG Lys 800	CGG Arg	CCC Pro	ATC Ile	GAC Asp 805	CTG Leu	GCG Ala	TTG Leu	CTG Leu	CAG Gln	TTC Phe 810	CTG Leu	GGG Gly	GAT Asp	GAT Asp	GAG Glu 815	2929
ATC Ile	GAG Glu	ATG Met	CTG Leu	GAG Glu 820	CGG Arg	CTG Leu	TGG Trp	CTC Leu	TCT Ser	GGG Gly 825	ATC Ile	TGC Cys	CAC His	AAT Asn 830	GAC Asp	2977
AAA Lys	ATC Ile	GAG Glu	GTG Val 835	ATG Met	AGC Ser	AGC Ser	AAG Lys	CTG Leu 840	GAC Asp	ATC Ile	GAC Asp	AAC Asn 845	ATG Met	GCG Ala	GGC Gly	3025
GTC Val	TTC Phe 850	TAC Tyr	ATG Met	CTC Leu	CTG Leu	GTG Val	GCC Ala 855	ATG Met	GGC Gly	CTG Leu	TCC Ser	CTG Leu	CTG Leu	GTC Val	TTC Phe	3073
GCC Ala 865	TGG Trp	GAG Glu	CAC His	CTG Leu	GTG Val	TAC Tyr 870	TGG Trp	CGC Arg	CTG Leu	CGG Arg	CAC His 875	TGC Cys	CTG Leu	GGG Gly	CCC Pro	3121
ACC Thr 880	CAC His	CGC Arg	ATG Met	GAC Asp 885	TTC Phe	CTG Leu	CTG Leu	GCC Ala	TTC Phe	TCC Ser 890	AGG Arg	GGC Gly	ATG Met	TAC Tyr	AGC Ser 895	3169
TGC Cys	TGC Cys	AGC Ser	GCT Ala	GAG Glu 900	GCC Ala	GCC Ala	CCA Pro	CCG Pro	CCC Pro	GCC Ala 905	AAG Lys	CCC Pro	CCG Pro	CCG Pro	CCG Pro	3217
CCA Pro	CAG Gln	CCC Pro	CTG Leu 915	CCC Pro	AGC Ser	CCC Pro	GCG Ala	TAC Tyr 920	CCC Pro	GCG Ala	CCG Pro	GGG Gly	CCG Pro	GCT Ala	CCC Pro	3265
GGG Gly	CCC Pro	GCA Ala 930	CCT Pro	TTC Phe	GTC Val	CCC Pro	CGC Arg	GAG Glu	CGC Arg	GCC Ala	TCA Ser	GTG Val 940	GCC Ala	CGC Arg	TGG Trp	3313
CGC Arg	CGG Arg	CCC Pro	AAG Lys	GGC Gly	GCG Ala	GGG Gly 950	CCG Pro	CCG Pro	GGG Gly	GGC Gly	GCG Ala 955	GGC Gly	CTG Leu	GCC Ala	GAC Asp	3361
GGC Gly 960	TTC Phe	CAC His	CGC Arg	TAC Tyr	TAC Tyr 965	GGC Gly	CCC Pro	ATC Ile	GAG Glu	CCG Pro 970	CAG Gln	GGC Gly	CTA Leu	GGC Gly	CTC Leu 975	3409
GGC Gly	CTG Leu	GGC Gly	GAA Glu	GCG Ala 980	CGC Arg	GCG Ala	GCA Ala	CCG Pro	CGG Arg 985	GGC Gly	GCA Ala	GCC Ala	GGG Gly	CGC Arg	CCG Pro 990	3457

CTG TCC CCG CCG GCC GCT CAG CCC CCG CAG AAG CCG CCG GCC TCC TAT Leu Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr 995 1000 1005	3505
TTC GCC ATC GTA CGC GAC AAG GAG CCA GCC GAG CCC CCC GCC GGC GCC Phe Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala 1010 1015 1020	3553
TTC CCC GGC TTC CCG TCC CCG CCC GCG CCC CCC GCC GCC GCG GCC ACC Phe Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Thr 1025 1030 1035	3601
GCC GTC GGG CCG CCA CTC TGC CGC TTG GCC TTC GAG GAC GAG AGC CCG Ala Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro 1040 1045 1050 1055	3649
CCG GCG CCC GCG CCG TGG CCG CCG TCG GAC CCC GAG AGC CAA CCC CTG Pro Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu 1060 1065 1070	3697
CTG GGG CCA GGC GCG GGC GGC GCG GGG GGC ACG GGG GGC GCA GGC GGA Leu Gly Pro Gly Ala Gly Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly 1075 1080 1085	3745
GGA GCC CCG GCC GCT CCG CCC CCG TGC TTC GCC GCG CCG CCC CCG TGC Gly Ala Pro Ala Ala Pro Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys 1090 1095 1100	3793
TTT TAC CTC GAT GTC GAC CAG TCG CCG TCG GAC TCG GAG GAC TCG GAG Phe Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu 1105 1110 1115	3841
AGC CTG GCC GGC GCG TCC CTG GCC GGC CTG GAT CCC TGG TGG TTC GCC Ser Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala 1120 1125 1130 1135	3889
GAC TTC CCT TAC CCG TAT GCC GAT CGC CTC GGG CSG CCC GCG GCA CGC Asp Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg 1140 1145 1150	3937
TAC GGA TTG GTC GAC AAA CTA GGG GGC TGG CTC GCC GGG AGC TGG GAC Tyr Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp 1155 1160 1165	3985
TAC CTG CCT CCS CGC AGC GGT CGG GCC GCC TGG CAC TGT CGG CAC TGC Tyr Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys 1170 1175 1180	4033
GCC AGC CTG GAG CTG CTT CCG CCG CCG CGC CAT CTC AGC TGC TCG CAC Ala Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His 1185 1190 1195	4081
GAT GGC CTG GAC GGC GGC TGG TGG GCG CCA CCG CCT CCA CCC TGG GCC Asp Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Pro Trp Ala 1200 1205 1210 1215	4129
GCC GGG CCC CTG CCC CGA CGC CGG GCC CGC TGC GGG TGC CCG CGG TCG Ala Gly Pro Leu Pro Arg Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser 1220 1225 1230	4177
CAC CCG CAC CGC CCG CGG GCC TCG CAC CGC ACG CCC GCC GCT GCC GCG His Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala Ala 1235 1240 1245	4225
CCC CAC CAC CAC AGG CAC CGG CGC GCC GCT GGG GGC TGG GAC CTC CCG Pro His His His Arg His Arg Arg Ala Ala Gly Gly Trp Asp Leu Pro 1250 1255 1260	4273

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CCG CCC GCG CCC ACC TCG CGC TCG CTC GAG GAC CTC AGC TCG TGC CCT 4321
 Pro Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro
 1265 1270 1275

CGC GCC GCC CCT GCG CGC AGG CTT ACC GGG CCC TCC CGC CAC GCT CGC 4369
 Arg Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg
 1280 1285 1290 1295

AGG TGT CCG CAC GCC GCG CAC TGG GGG CCG CCG CTG CCT ACA GCT TCC 4417
 Arg Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser
 1300 1305 1310

CAC CGG AGA CAC CGG GGC GGG GAC CTG GGC ACC CGC AGG GGC TCG GCG 4465
 His Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala
 1315 1320 1325

CAC TTC TCT AGC CTC GAG TCC GAG GTA TGACGCGGCC CCGGGGGGCC 4512
 His Phe Ser Ser Leu Glu Ser Glu Val
 1330 1335

CACCGCCCCC TTGGTCAGCG CAGGCCACGG CCCGAGGGGG CGCCCGCAGT GGACAGGACC 4572

CGCGTGGGTT GGAAGGAAA GCAGTGAAC TGGCCGGACC CCGCCTGGAG CAGCGTCCTG 4632

CGCCCCCTGG TTCTGGAGGA ACCGCAAGCC GGAGAGGATT TGGTCCCTCA ACTATCACCC 4692

AGG 4695

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1336 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys Met
 1 5 10 15

Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu Ala
 20 25 30

Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly Ala
 35 40 45

Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala Ala
 50 55 60

Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Val Arg Ser Pro
 65 70 75 80

Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp Pro
 85 90 95

Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg Val
 100 105 110

His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala Pro
 115 120 125

Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser Glu
 130 135 140

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His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser Thr
 145 150 155 160
 Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile Phe
 165 170 175
 Glu Val Leu Glu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr Thr
 180 185 190
 Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu Thr
 195 200 205
 Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu Asp
 210 215 220
 Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val Ser
 225 230 235 240
 Ala Gln Ile Arg Leu Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro Val
 245 250 255
 Phe Arg Ala Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val Trp
 260 265 270
 Phe Met Val Gly Pro Gln Leu Ala Gly Gly Gly Gly Ser Gly Ala Pro
 275 280 285
 Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly Leu
 290 295 300
 Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg Val
 305 310 315 320
 Ala Ala Gly Val Ala Val Val Ala Arg Gly Ala Gln Ala Leu Leu Arg
 325 330 335
 Asp Tyr Gly Phe Leu Pro Glu Leu Gly His Asp Cys Arg Ala Gln Asn
 340 345 350
 Arg Thr His Arg Gly Glu Ser Leu His Arg Tyr Phe Met Asn Ile Thr
 355 360 365
 Trp Asp Asn Arg Asp Tyr Ser Phe Asn Glu Asp Gly Phe Leu Val Asn
 370 375 380
 Pro Ser Leu Val Val Ile Ser Leu Thr Arg Asp Arg Thr Trp Glu Val
 385 390 395 400
 Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu Trp
 405 410 415
 Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His Leu
 420 425 430
 Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro Ala
 435 440 445
 Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg Ser
 450 455 460
 Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro Glu
 465 470 475 480
 Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu Ala
 485 490 495

His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys
 500 505 510
 His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu Val
 515 520 525
 Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn Glu
 530 535 540
 Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly
 545 550 555 560
 Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser Ala
 565 570 575
 Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val Met
 580 585 590
 Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu Ser
 595 600 605
 Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly Gly
 610 615 620
 Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu Val
 625 630 635 640
 Phe Asn Asn Ser Val Pro Val Glu Asn Pro Arg Gly Thr Thr Ser Lys
 645 650 655
 Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser
 660 665 670
 Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp
 675 680 685
 Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu Gln
 690 695 700
 Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Lys
 705 710 715 720
 Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg Tyr
 725 730 735
 Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly Lys
 740 745 750
 Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Arg
 755 760 765
 Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe
 770 775 780
 Ala Thr Thr Gly Tyr Gly Ile Ala Leu His Lys Gly Ser Arg Trp Lys
 785 790 795 800
 Arg Pro Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Asp Glu Ile
 805 810 815
 Glu Met Leu Glu Arg Leu Trp Leu Ser Gly Ile Cys His Asn Asp Lys
 820 825 830
 Ile Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly Val
 835 840 845

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Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ser Leu Leu Val Phe Ala
 850 855 860
 Trp Glu His Leu Val Tyr Trp Arg Leu Arg His Cys Leu Gly Pro Thr
 865 870 875 880
 His Arg Met Asp Phe Leu Leu Ala Phe Ser Arg Gly Met Tyr Ser Cys
 885 890 895
 Cys Ser Ala Glu Ala Ala Pro Pro Pro Ala Lys Pro Pro Pro Pro Pro
 900 905 910
 Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro Gly
 915 920 925
 Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp Arg
 930 935 940
 Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp Gly
 945 950 955 960
 Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu Gly
 965 970 975
 Leu Gly Glu Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro Leu
 980 985 990
 Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr Phe
 995 1000 1005
 Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala Phe
 1010 1015 1020
 Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Ala Thr Ala
 1025 1030 1035 1040
 Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro Pro
 1045 1050 1055
 Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu Leu
 1060 1065 1070
 Gly Pro Gly Ala Gly Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly Gly
 1075 1080 1085
 Ala Pro Ala Ala Pro Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys Phe
 1090 1095 1100
 Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu Ser
 1105 1110 1115 1120
 Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala Asp
 1125 1130 1135
 Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg Tyr
 1140 1145 1150
 Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp Tyr
 1155 1160 1165
 Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys Ala
 1170 1175 1180
 Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His Asp
 1185 1190 1195 1200

1000747
 120701

Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Pro Trp Ala Ala
1205 1210 1215

Gly Pro Leu Pro Arg Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser His
1220 1225 1230

Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala Ala Pro
1235 1240 1245

His His His Arg His Arg Arg Ala Ala Gly Gly Trp Asp Leu Pro Pro
1250 1255 1260

Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro Arg
1265 1270 1275 1280

Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg Arg
1285 1290 1295

Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser His
1300 1305 1310

Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala His
1315 1320 1325

Phe Ser Ser Leu Glu Ser Glu Val
1330 1335

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGTGGCGGC CGCAGAGCAC CTCCACCATC TCCTTGTCTT ACTCCAAGAT CTGGCCCTAG 60
TCCATGTTTG C 71

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGGTGGTCCC CAACCTGTAG GACTTGGTTC TGGAGGAGGA TCTGGTGTAG GCAAACATGG 60
ACTAGGGCCA G 71

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(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTTGGGGACC ACCAGATGGA GGTAGAGCTG CACTTGTACG AAGAGCTCCA CAACCACCTG 60
 G 61

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGTGAGACGT CAGACAAAGG AGGCCCAGGT GTAGGTGGTC TACCAGGTGG TTGTGGAGCT 60
 CT 62

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 195 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGCAGAGCA CCTCCACCAT CTCCTTGTCC TACTCCAAGA TCTGGCCCTA GTCCATGTTT 60
 GCCTACACCA GATCCTCCTC CAGAACCAAG TCCTACAGGT TGGGGACCAC CAGATGGAGG 120
 TAGAGCTGCA CTTGTACGAA GAGCTCCACA ACCACCTGGT AGACCACCTA CACCTGGGCC 180
 TCCTTTGTCT GACGT 195

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